

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 11, 2005, 01:19:58 ; Search time 258 Seconds
(without alignments)
269.833 Million cell updates/sec

Title: US-09-529-206E-4
Perfect score: 959
Sequence: 1 MQAERGVTGGTGADAGPGG.....WITQCFLPVFLAQPSPGQRR 180

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*
1: Geneseqp1980s:*
2: Geneseqp1990s:*
3: Geneseqp2000s:*
4: Geneseqp2001s:*
5: Geneseqp2002s:*
6: Geneseqp2003as:*
7: Geneseqp2003bs:*
8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	959	100.0	180	2	AAW62584 Cancer as
2	959	100.0	180	2	Aaw69665 Human NY-
3	959	100.0	180	2	Aay05965 Human can
4	959	100.0	180	3	Aay52430 Human tum
5	959	100.0	180	3	Aay70862 Human tum
6	959	100.0	180	3	Aab03154 Human oes
7	959	100.0	180	4	Aab69946 Human NY-
8	959	100.0	180	4	Aag67164 Amino aci
9	959	100.0	180	4	Aau01535 Human NY-
10	959	100.0	180	4	Aae07714 Human NY
11	959	100.0	180	5	Aau84818 Human NYN
12	959	100.0	180	5	Aau11543 Human tum
13	959	100.0	180	6	Abr58672 Human can
14	959	100.0	180	6	Abr48210 Human bla
15	959	100.0	180	6	Abu56508 Lung canc
16	959	100.0	180	6	Abu56694 Lung canc
17	959	100.0	180	6	Abp74198 Human NY
18	959	100.0	180	6	Abr83438 Human NY-
19	959	100.0	180	7	Adc09576 NY-ESO-1
20	959	100.0	180	7	Add35568 Human NY-
21	959	100.0	180	7	Adp25510 Binding d
22	959	100.0	180	7	Adn39068 Cancer/an
23	959	100.0	180	8	Adj54139 Human NY-
24	959	100.0	180	8	Adm72815 Human NY-
25	959	100.0	180	8	Adq18451 Human sof

26	959	100.0	180	8	ADQ10446	Adq10446 Autoimmun
27	959	100.0	397	4	AAE13122	AAe13122 NY-ESO-1C
28	953	99.4	180	6	ABU64816	ABu64816 Human NY-
29	950	99.1	180	8	ADM73418	Adm73418 CAG-3 pro
30	950	99.1	180	8	ADM73417	Adm73417 Human NY-
31	934.5	97.4	179	8	ADK68648	Adk68648 Epitope 1
32	918	95.7	180	7	ADD35564	Add35564 Human NY-
33	821	85.6	180	6	ABP74199	Abp74199 Human LAG
34	821	85.6	180	7	ADC09577	Adc09577 LAGE-1a p
35	821	85.6	180	8	ADM72816	Adm72816 Human LAG
36	814	84.9	180	2	Aaw69664	Aaw69664 Human LAG
37	814	84.9	180	3	AAW70860	Aaw70860 Human LAG
38	814	84.9	180	5	AAU84820	Aau84820 Human LAG
39	814	84.9	180	5	ABB78346	Abb78346 Amino aci
40	814	84.9	180	7	ADC35103	Adc35103 Human bre
41	814	84.9	188	8	ADR66117	Adr66117 Human pro
42	814	84.9	188	8	ADR66459	Adr66459 Human pro
43	813	84.8	180	8	ADM73419	Adm73419 LAGE-1a p
44	808.5	84.3	179	8	ADM73424	Adm73424 Consensus
45	806	84.0	180	8	ADM73420	Adm73420 LAGE-1a p

ALIGNMENTS

RESULT 1
AAW62584
ID AAW62584 standard; protein; 180 AA.
XX
AC AAW62584;
XX
DT 17-SEP-1998 (first entry)
XX
DE Cancer associated antigen NY-ESO-1.
XX
KW Cancer associated antigen; NY-ESO-1; regression; progression; onset;
KW cancer; treatment; diagnosis.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Misc-difference 7 /note= "potential myristoylation site"
FT Misc-difference 9 /note= "potential myristoylation site"
FT Misc-difference 11 /note= "potential phosphorylation site"
FT Misc-difference 98 /note= "potential phosphorylation site"
FT Misc-difference 134 /note= "potential phosphorylation site"
FT Misc-difference 138 /note= "potential phosphorylation site"
XX
WO9814464-A1.
09-APR-1998.
15-SEP-1997; 97WO-US016335.
03-OCT-1996; 96US-00725182.
(LUDW-) LUDWIG INST CANCER RES.
Chen Y, Scanlan M, Gure A, Old LJ, Jager E, Knuth A;
Drifflouth JW;
WPI; 1998-286417/25.
N-PSDB; AAV38566.
New isolated cancer associated antigen - is used to develop products for
the diagnosis and treatment of cancers and for monitoring cancer therapy.

PS Claim 8; Fig 3; 49pp; English.

XX The present sequence represents a cancer associated antigen. The clone from which the DNA sequence is obtained is designated NY-ESO-1. The specification described a method for determining regression, progression of onset of a cancerous condition, comprising monitoring a sample from a patient with the cancerous condition for a parameter selected from NY-ESO-1 protein, a peptide derived from NY-ESO-1 protein and cytolytic T cells specific for the peptide and an MHC molecule with which it non-covalently complexes. Methods for the treatment of a cancerous condition are also described. The NY-ESO-1 protein and peptides derived from it can be used for diagnosis and treatment of cancers and to monitor the efficacy of a therapeutic regime

XX Sequence 180 AA;

SQ Query Match 100.0%; Score 959; DB 2; Length 180;
 Best Local Similarity 100.0%; Pred. No. 5.2e-79;
 Matches 180; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MQAEGRTGSGTGDADGPGGPGIPDGGNAGGPGGAGATGGRGPRGAGAAASGPGGGA 60
 |||||
 DB 1 MQAEGRTGSGTGDADGPGGPGIPDGGNAGGPGGAGATGGRGPRGAGAAASGPGGGA 60
 |||||

QY 61 PRGPHGGAASGLNGCCRCGARGPESRLLEFYLLAMPFATPMEAEALARRSLAQDAPPLVPVG 120
 |||||
 DB 61 PRGPHGGAASGLNGCCRCGARGPESRLLEFYLLAMPFATPMEAEALARRSLAQDAPPLVPVG 120
 |||||

QY 121 VLLKEFTVSGNIIITRLTAADHRQLQLSISSCLQLSLLMWITQCFPLVFLAQPSPGQRR 180
 |||||
 DB 121 VLLKEFTVSGNIIITRLTAADHRQLQLSISSCLQLSLLMWITQCFPLVFLAQPSPGQRR 180
 |||||

RESULT 2

AAW69665

ID AAW69665 standard; protein; 180 AA.

AC AAW69665;

XX 27-OCT-1998 (first entry)

DT Human NY-ESO-1 protein sequence, formerly known as LL-1.2 clone.

DE Human; LAGE-1; tumour associated protein; LL-1; diagnosis; tumour.

XX Homo sapiens.

OS WO9832855-A1.

PN 30-JUL-1998.

PD 27-JAN-1998; 98WO-US001445.

PF 27-JAN-1997; 97US-00791495.

PR (LUDW-) LUDWIG INST CANCER RES.

PA Lethe B, Lucas S, De Smet C, Godelaine D, Boon-Falleur T;

PI WPI; 1998-427951/36.

DR N-PSDB; AAV50348.

XX New isolated LAGE-1 tumour associated nucleic acids - used to develop products for the diagnosis and treatment of LAGE-1 associated disorders, particularly tumours.

PS Example 2; Page 57-58; 73pp; English.

XX The present sequence represents human NY-ESO-1, formerly known as LL-1.2 clone, which is used in an example from the present invention which describes LAGE-1 tumour associated protein (TAP). The present invention also describes: (1) a method for treating a subject with a disorder characterised by expression of a LAGE-1 nucleic acid molecule or an

CC expression product, comprising administering to the subject autologous cytolytic T cells to ameliorate the disorder, where the cytolytic T cells are specific for complexes of an HLA molecule and a LAGE-1 TAP or an immunogenic fragment; (2) a method for treating a subject with a disorder characterised by expression of a LAGE-1 nucleic acid molecule or an expression product, comprising administering a LAGE-1 TAP or an immunogenic fragment to ameliorate the disorder; and (3) a method for selectively enriching a population of T cells with cytolytic T cells specific for a LAGE-1 TAP comprising contacting an isolated population of T cells with an agent presenting a complex of a LAGE TAP or an immunogenic fragment and a HLA presenting molecule to selectively enrich the isolated population of T cells with the cytolytic T cells. The methods and products from the present invention can be used for the diagnosis and treatment of LAGE-1 associated disorders, particularly tumours

XX Sequence 180 AA;

SQ Query Match 100.0%; Score 959; DB 2; Length 180;
 Best Local Similarity 100.0%; Pred. No. 5.2e-79;
 Matches 180; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MQAEGRTGSGTGDADGPGGPGIPDGGNAGGPGGAGATGGRGPRGAGAAASGPGGGA 60
 |||||
 DB 1 MQAEGRTGSGTGDADGPGGPGIPDGGNAGGPGGAGATGGRGPRGAGAAASGPGGGA 60
 |||||

QY 61 PRGPHGGAASGLNGCCRCGARGPESRLLEFYLLAMPFATPMEAEALARRSLAQDAPPLVPVG 120
 |||||
 DB 61 PRGPHGGAASGLNGCCRCGARGPESRLLEFYLLAMPFATPMEAEALARRSLAQDAPPLVPVG 120
 |||||

QY 121 VLLKEFTVSGNIIITRLTAADHRQLQLSISSCLQLSLLMWITQCFPLVFLAQPSPGQRR 180
 |||||
 DB 121 VLLKEFTVSGNIIITRLTAADHRQLQLSISSCLQLSLLMWITQCFPLVFLAQPSPGQRR 180
 |||||

RESULT 3

AAW05965

ID AAY05965 standard; protein; 180 AA.

XX AAY05965;

XX 16-AUG-1999 (first entry)

DT Human cancer antigen NY ESO-1/CAG-3 ORF1 protein.

DE NY ESO-1/CAG-3 gene; CAG-3 gene; cancer antigen; human; leukaemia; non-Hodgkins lymphoma; Hodgkins lymphoma; lung cancer; metastasis; melanoma; adenocarcinoma; thymoma; colon cancer; uterine cancer; breast cancer; prostate cancer; ovarian cancer; cervical cancer; bladder cancer; kidney cancer; pancreatic cancer; liver cancer; sarcoma; tumour; diagnosis; immunotherapy; therapy; vaccine; ORF1.

XX Homo sapiens.

OS WO9918206-A2.

PN 15-APR-1999.

PD 21-SEP-1998; 98WO-US019609.

PF 08-OCT-1997; 97US-0061428P.

PR (USSH) US DEPT HEALTH & HUMAN SERVICES.

PA Wang RF, Rosenberg SA;

PI WPI; 1999-277270/23.

DR N-PSDB; AAY58599.

XX Cancer antigen NY ESO1/CAG-3.

PS Claim 4; Fig 3A; 88pp; English.

XX

CC The present sequence represents the ORF1 protein encoded by open reading
 CC frame 1 of the human ESO-1/CAG-3 (or CAG-3) gene. CAG-3 is a new and
 CC potent tumour antigen capable of eliciting an antigen specific immune
 CC response by T cells. Cancer peptides comprising ORF1, ORF2 (see
 CC AAY05966), portions of these peptides and their variants (see AAY05965-
 CC 87), are useful as cancer vaccines that protect the recipient from
 CC development of cancer. The invention provides: vectors and host cells
 CC (also useful as vaccines); a method of diagnosis of cancer or precancer;
 CC a transgenic animal; antisense oligonucleotides that inhibit expression
 CC of the cancer peptide or tumour antigen; antibodies reacting with the CAG
 CC -3 cancer peptide, useful in diagnostic and detection assays; and methods
 CC for preventing or inhibiting cancer by administering a cancer peptide,
 CC with or without an HLA molecule. The cancer peptides form part of, or are
 CC derived from, cancers such as primary or metastatic melanoma, thymoma,
 CC lymphoma, sarcoma, lung cancer, liver cancer, leukaemia, uterine cancer,
 CC cervical cancer, bladder cancer, kidney cancer and adenocarcinomas such
 CC as breast, prostate, ovarian, pancreatic and thyroid cancers. Melanoma is
 CC treated by inducing cancer-specific T cells in vitro for subsequent
 CC return to a patient
 XX
 SQ Sequence 180 AA;

Query Match 100.0%; Score 959; DB 2; Length 180;
 Best Local Similarity 100.0%; Pred. No. 5.2e-79;
 Matches 180; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MQAEGRTGSGTGDADGPGGPGIPDGGNAGGPGGAGATGGRPGAGAAASGPGGGA 60
 DB 1 MQAEGRTGSGTGDADGPGGPGIPDGGNAGGPGGAGATGGRPGAGAAASGPGGGA 60
 QY 61 PRPHGGAASGLNGCCRCGARGPESRLLEPYLAMPATPWEALARRSLAQDAPPLPVFG 120
 DB 61 PRPHGGAASGLNGCCRCGARGPESRLLEPYLAMPATPWEALARRSLAQDAPPLPVFG 120
 QY 121 VLLKFTVSGNLTIRLTADHRQLQLSSCLQLSLMWITQCFPLVFLAQPSSGQR 180
 DB 121 VLLKFTVSGNLTIRLTADHRQLQLSSCLQLSLMWITQCFPLVFLAQPSSGQR 180

RESULT 4

AAY52430
 ID AAY52430 standard; protein; 180 AA.

AC AAY52430;
 DT 21-OCT-2004 (revised)
 DT 15-FEB-2000 (first entry)
 DE Human tumour antigen NY-ESO-1.
 XX
 XX Cancer; tumour; antigen; MHC; major histocompatibility complex; T-cell;
 KW cytotoxic; helper; stimulation; proliferation; treatment; diagnosis;
 KW prevention; melanoma; breast cancer; ovarian cancer; prostate cancer;
 KW hepatoma; thyroid cancer; bladder cancer; lung cancer; lymphoma.

OS Homo sapiens.
 OS Unidentified.

FH Key Location/Qualifiers

FT Peptide 44..53
 FT /note= "Peptide presented by MHC Class I HLA-B7"
 FT Peptide 60..69
 FT /note= "Peptide presented by MHC Class I HLA-B7"
 FT Peptide 60..68
 FT /note= "Peptide presented by MHC Class I HLA-B7"
 FT Peptide 63..72
 FT /note= "Peptide presented by MHC Class I HLA-B7"
 FT Peptide 79..88
 FT /note= "Peptide presented by MHC Class I HLA-B7"
 FT Peptide 79..87
 FT /note= "Peptide presented by MHC Class I HLA-B7, HLA-B8
 FT and HLA-B35"
 FT Peptide 82..91

FT Peptide
 FT /note= "Peptide presented by MHC Class I HLA-A1"
 FT 82..90
 FT /note= "Peptide presented by MHC Class I HLA-A1"
 FT 83..91
 FT /note= "Peptide presented by MHC Class I HLA-B44"
 FT 84..92
 FT /note= "Peptide presented by MHC Class I HLA-B7, HLA-B8
 FT and HLA-B35"
 FT 87..96
 FT /note= "Peptide presented by MHC Class I HLA-A1"
 FT 88..96
 FT /note= "Peptide presented by MHC Class I HLA-B44"
 FT 96..104
 FT /note= "Peptide presented by MHC Class I HLA-B7"
 FT 100..108
 FT /note= "Peptide presented by MHC Class I HLA-B44"
 FT 102..110
 FT /note= "Peptide presented by MHC Class I HLA-B44"
 FT 107..116
 FT /note= "Peptide presented by MHC Class I HLA-A24"
 FT 110..118
 FT /note= "Peptide presented by MHC Class I HLA-B52"
 FT 113..122
 FT /note= "Peptide presented by MHC Class I HLA-B7 and HLA-
 FT B52"
 FT 113..121
 FT /note= "Peptide presented by MHC Class I HLA-B7"
 FT 115..124
 FT /note= "Peptide presented by MHC Class I HLA-A3"
 FT 118..126
 FT /note= "Peptide presented by MHC Class I HLA-B35"
 FT 124..133
 FT /note= "Peptide presented by MHC Class I HLA-B52"
 FT 125..133
 FT /note= "Peptide presented by MHC Class I HLA-A24"
 FT 138..147
 FT /note= "Peptide presented by MHC Class I HLA-B8"
 FT 139..147
 FT /note= "Peptide presented by MHC Class I HLA-B7"
 FT 145..153
 FT /note= "Peptide presented by MHC Class I HLA-A24 and HLA-
 FT B52"
 FT 153..162
 FT /note= "Peptide presented by MHC Class I HLA-B52"
 FT 154..163
 FT /note= "Peptide presented by MHC Class I HLA-B52"
 FT 154..162
 FT /note= "Peptide presented by MHC Class I HLA-B52"
 FT 156..167
 FT /note= "Peptide (AAY52434) presented by MHC Class I HLA-
 FT A2"
 FT 158..166
 FT /note= "Peptide presented by MHC Class I HLA-A3"
 FT 159..167
 FT /note= "Peptide presented by MHC Class I HLA-A3"
 FT 162..170
 FT /note= "Peptide presented by MHC Class I HLA-B52"
 FT
 XX WO959398-A1.
 XX
 PD 28-OCT-1999.
 XX
 PF 24-MAR-1999;
 XX 99WO-US006875.
 PR 17-APR-1998;
 PR 98US-00062422.
 PR 02-OCT-1998;
 PR 98US-00165546.
 XX (LUDW-) LUDWIG INST CANCER RES.
 XX
 PI Stockert E, Jager E, Chen Y, Scanlan M, Alexander K, Old LJ;
 PI Gure A, Ritter G;
 XX
 DR WPI; 2000-038483/03.

DR N-PSDB; AAZ38380.
XX
XX Novel peptides which bind to MHC class I and MHC class II molecules,
PT useful for therapeutic and diagnostic purposes.
XX
XX Claim 30; Fig 3; 49pp; English.
XX
XX This sequence represents a human tumour antigen, NY-ESO-1, the cDNA
CC encoding which was isolated from an oesophagus squamous cell cancer cDNA
CC library. Tissue localisation studies revealed it to be expressed at high
CC levels in normal ovary and testis but not in normal colon, kidney, liver,
CC brain, oesophagus and skin. It was expressed in certain tumours and
CC tumour cell lines with some degree of frequency - these included melanoma
CC specimens and cell lines, and breast and bladder cancer specimens, with
CC expression in other tumour types being sporadic. Peptides derived from NY
CC -ESO-1 are bound by both MHC (major histocompatibility complex) Class I
CC and Class II molecules for presentation to T-cells. Peptides AAY52431-
CC Y52434 bind to Class I HLA-A2 molecules, thereby stimulating
CC proliferation of cytotoxic T-cells, while peptides AAY52435-Y52440 bind
CC to Class II HLA-DR33 molecules, stimulating helper T-cell proliferation.
CC The peptides derived from NY-ESO-1 may be used in methods and
CC compositions used for the treatment, diagnosis and prevention of cancers
CC (such as melanoma, breast cancer, prostate cancer, lung cancer, hepatoma,
CC ovarian cancer, thyroid cancer, bladder cancer, or lymphoma) and to
CC stimulate the proliferation of T cells
CC
XX Revised record issued on 21-OCT-2004 : Correction to feature table key
XX
SQ Sequence 180 AA;

Query Match 100.0%; Score 959; DB 3; Length 180;
Best Local Similarity 100.0%; Pred. No. 5.2e-79;
Matches 180; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MQAEGRTGSGTGDADGPGGPIPDGPGNAGGPGGAGATGGRGAGAAASGPGGGA 60
DB 1 MQAEGRTGSGTGDADGPGGPIPDGPGNAGGPGGAGATGGRGAGAAASGPGGGA 60

QY 61 PRGPHGGAASGLNGCCRCGARGPESRLLEFYLLAMPFATPMEAEIARRSLAQDAPPLVPVG 120
DB 61 PRGPHGGAASGLNGCCRCGARGPESRLLEFYLLAMPFATPMEAEIARRSLAQDAPPLVPVG 120

QY 121 VLLKEFTVSGNLTIRLTAADHRQLQLSISSCLQLSLLMWITQCFLPVFLAQPPSGQRR 180
DB 121 VLLKEFTVSGNLTIRLTAADHRQLQLSISSCLQLSLLMWITQCFLPVFLAQPPSGQRR 180

RESULT 5
AAY70862
ID AAY70862 standard; protein; 180 AA.
XX
XX AAY70862;
XX
XX 31-JUL-2000 (first entry)
XX
XX Human tumour antigen, NY-ESO-1 protein.
DE
XX NY-ESO-1; CAMEL; CTL-recognised Antigen on MELANOMA; human; cancer; CTL;
KW cytotoxic T lymphocyte; tumour-associated antigen; LAGE-1; anticancer;
KW melanoma; immunotherapy; immune response.
XX
XX Homo sapiens.
XX
XX WO200023584-A1.
XX
XX 27-APR-2000.
XX
XX 15-OCT-1999; 99WO-EP007832.
XX
XX 16-OCT-1998; 98EP-00119583.
XX
XX (BOEH) BOEHRINGER INGELHEIM INT GMBH.
PA (UYHO-) UNIV HOSPITAL LEIDEN.

XX Schrier PI, Aarnoudse CA, Heider K, Klade C;
XX WPI; 2000-339685/29.
XX N-PSDB; AAD00152.
XX
XX Tumor-associated antigen useful for cancer immunotherapy is encoded by
PT the open reading frame of LAGE-1 (a tumor-specific antigen) cDNA.
XX
XX Example 3; Page 62-63; 73pp; English.
XX
XX The present sequence is the human NY-ESO-1 protein, a tumour antigen,
CC identified by screening an esophagus carcinoma cDNA library. This protein
CC is derived from open reading frame (ORF)-1 that contain epitopes of
CC tumour specific T-cells. NY-ESO-1 is expressed in different tumour types,
CC but not in healthy tissues except in testis. It also shows homology with
CC the CAMEL (Cytotoxic T lymphocytes (CTL)-recognised Antigen on MELANOMA)
CC protein, a tumour-associated antigen. The tumour-associated antigen
CC displayed on melanoma cells is recognised by cytotoxic T lymphocytes.
CC This sequence has anticancer activity. CAMEL tumour antigen and
CC immunogenic peptides derived from it are useful for cancer immunotherapy.
CC They have the potential to induce an immune response, by eliciting a CTL
CC response. The DNA molecule is used for the construction of recombinant or
CC fusion proteins
XX
XX Sequence 180 AA;
SQ

Query Match 100.0%; Score 959; DB 3; Length 180;
Best Local Similarity 100.0%; Pred. No. 5.2e-79;
Matches 180; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MQAEGRTGSGTGDADGPGGPIPDGPGNAGGPGGAGATGGRGAGAAASGPGGGA 60
DB 1 MQAEGRTGSGTGDADGPGGPIPDGPGNAGGPGGAGATGGRGAGAAASGPGGGA 60

QY 61 PRGPHGGAASGLNGCCRCGARGPESRLLEFYLLAMPFATPMEAEIARRSLAQDAPPLVPVG 120
DB 61 PRGPHGGAASGLNGCCRCGARGPESRLLEFYLLAMPFATPMEAEIARRSLAQDAPPLVPVG 120

QY 121 VLLKEFTVSGNLTIRLTAADHRQLQLSISSCLQLSLLMWITQCFLPVFLAQPPSGQRR 180
DB 121 VLLKEFTVSGNLTIRLTAADHRQLQLSISSCLQLSLLMWITQCFLPVFLAQPPSGQRR 180

RESULT 6
AAB03154
ID AAB03154 standard; protein; 180 AA.
XX
XX AAB03154;
XX
XX 23-OCT-2000 (first entry)
XX
XX Human oesophageal cancer-associated antigen NY-ESO-1.
XX
XX Oesophageal cancer associated antigen; NY-ESO-1; human; immunogen;
KW oesophageal carcinoma; melanoma; ovary; testis; transmembrane domain;
KW antibody; diagnostic marker; drug delivery target.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
FH Modified-site 7
FT /note= "Potential N-myristoylation site"
FT Modified-site 9
FT /note= "Potential N-myristoylation site"
FT Modified-site 11
FT /note= "Potential O-phosphorylation site"
FT Modified-site 98
FT /note= "Potential O-phosphorylation site"
FT Modified-site 134
FT /note= "Potential O-phosphorylation site"
FT Modified-site 138
FT /note= "Potential O-phosphorylation site"
FT

FT Domain 152..172
 XX /note= "Potential transmembrane domain"
 PN US6069233-A.
 XX
 PD 30-MAY-2000.
 XX
 PF 26-JAN-1998; 98US-00013150.
 XX
 PR 03-OCT-1996; 96US-00725381.
 XX
 PA (SLOK) SLOAN KETTERING INST CANCER RES.
 PA (CORR) CORNELL RES FOUND INC.
 PA (LUDW-) LUDWIG INST CANCER RES.
 XX
 PI Scanlan M, Gure AO, Chen Y, Tureci O, Sahin U, Pfreundschuh M;
 PI Old LJ;
 XX
 DR WPI; 2000-410880/35.
 DR N-PSDB; AAA61483.
 XX
 PT New isolated esophageal cancer-associated antigen useful as markers for
 PT producing antibodies and as targets for identifying abnormal conditions,
 PT e.g. infections and cancer.
 XX
 XX Example 5; Fig 3; 9pp; English.
 XX
 CC This sequence represents a human oesophageal cancer-associated antigen,
 CC NY-ESO-1. The cDNA encoding this sequence was isolated from a cDNA
 CC library prepared from a specimen of well-to-moderately differentiated
 CC squamous cell cancer of the oesophagus. Expression analysis demonstrated
 CC that NY-ESO-1 was expressed in oesophageal carcinoma, certain melanoma
 CC cell lines and in normal ovary and testis tissue, but not in normal
 CC colon, kidney, liver or brain tissue. Analysis of the amino acid sequence
 CC of the protein indicates that the protein has a transmembrane domain,
 CC several N-myristoylation sites and O-phosphorylation sites and that it
 CC contains antigenic sequences in the N-terminal half of the protein. The
 CC antigen is useful as an immunogen when combined with an adjuvant, in both
 CC precursor and post- translationally modified forms, and may be used to
 CC generate anti-NY-ESO-1 antibodies. It can also be used as a diagnostic
 CC marker for oesophageal cancer, and can be utilised as a marker for the
 CC targeted delivery of therapeutic agents to oesophageal cancer cells. It
 CC can also be used to generate diagnostic or therapeutic agents
 XX
 SQ Sequence 180 AA;

Query Match 100.0%; Score 959; DB 3; Length 180;
 Best Local Similarity 100.0%; Pred. No. 5.2e-79;
 Matches 180; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MQAEGRTGGTGDADGGPGGIPDGGNAGGPGGAGATGGRGPRGAGAAASGPGGGA 60
 DB 1 MQAEGRTGGTGDADGGPGGIPDGGNAGGPGGAGATGGRGPRGAGAAASGPGGGA 60

QY 61 PRGPHGGAASGLNGCCRGARGPESRLLEFYLLAMPFATPMEAEIARRSLAQDAPPLVPVG 120
 DB 61 PRGPHGGAASGLNGCCRGARGPESRLLEFYLLAMPFATPMEAEIARRSLAQDAPPLVPVG 120

QY 121 VLLKEFTVSGNLTIRLTAAHRLQLSLSSCLQQLSLLMWITQCFLPFLAQPSPGQRR 180
 DB 121 VLLKEFTVSGNLTIRLTAAHRLQLSLSSCLQQLSLLMWITQCFLPFLAQPSPGQRR 180

RESULT 7
 AAB69946
 ID AAB69946 standard; protein; 180 AA.
 XX
 AC AAB69946;
 XX
 XX 27-APR-2001 (first entry)
 DT
 XX Human NY-ESO-1 protein.
 DE
 XX

KW Human; NY-ESO-1; HLA; human leukocyte antigen; CTL; cytotoxic T cell;
 KW HLA-A2; HLA-DR53; melanoma; adenocarcinoma; bladder carcinoma;
 KW non-small cell lung carcinoma; tumour status determination.
 XX
 OS Homo sapiens.
 XX
 PN WO200107917-A1.
 XX
 PD 01-FEB-2001.
 XX
 PF 14-JUL-2000; 2000WO-US019220.
 XX
 PR 23-JUL-1999; 99US-00359503.
 XX
 XX (LUDW-) LUDWIG INST CANCER RES.
 PA (SLOK) SLOAN KETTERING INST CANCER RES.
 PA (CORR) CORNELL RES FOUND INC.
 XX
 PI Jager E, Stockert E, Old LJ, Knuth A, Chen Y, Scanlan M;
 PI WPI; 2001-182822/18.
 DR N-PSDB; AAF58634.
 XX
 PT Method useful for determining the status (e.g. progression, regression or
 PT stability of the disease) of a cancerous condition, involves determining
 PT the levels of NY-ESO-1 specific antibodies in a sample taken from a
 PT patient.
 XX
 XX Example 5; Fig 3; 50pp; English.
 XX
 CC The present sequence is human NY-ESO-1 protein. It is provided in a
 CC specification relating to a method for determining the status of a
 CC cancerous condition in a patient with a tumour that expresses NY-ESO-1.
 CC The method comprises assaying a sample taken from the patient for
 CC antibodies that specifically bind to the NY-ESO-1 and comparing the value
 CC obtained to a prior value obtained from assay of a prior sample taken
 CC from the patient. Any difference between the values is indicative of a
 CC change in status of the cancerous condition. The method is useful for
 CC determining whether a cancerous condition is progressing, regressing or
 CC remaining stable, in particular in patients receiving treatment for a
 CC melanoma, adenocarcinoma, non-small cell lung carcinoma or bladder
 CC carcinoma
 XX
 SQ Sequence 180 AA;

Query Match 100.0%; Score 959; DB 4; Length 180;
 Best Local Similarity 100.0%; Pred. No. 5.2e-79;
 Matches 180; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MQAEGRTGGTGDADGGPGGIPDGGNAGGPGGAGATGGRGPRGAGAAASGPGGGA 60
 DB 1 MQAEGRTGGTGDADGGPGGIPDGGNAGGPGGAGATGGRGPRGAGAAASGPGGGA 60

QY 61 PRGPHGGAASGLNGCCRGARGPESRLLEFYLLAMPFATPMEAEIARRSLAQDAPPLVPVG 120
 DB 61 PRGPHGGAASGLNGCCRGARGPESRLLEFYLLAMPFATPMEAEIARRSLAQDAPPLVPVG 120

QY 121 VLLKEFTVSGNLTIRLTAAHRLQLSLSSCLQQLSLLMWITQCFLPFLAQPSPGQRR 180
 DB 121 VLLKEFTVSGNLTIRLTAAHRLQLSLSSCLQQLSLLMWITQCFLPFLAQPSPGQRR 180

RESULT 8
 AAG67164
 ID AAG67164 standard; protein; 180 AA.
 XX
 AC AAG67164;
 XX
 XX 13-NOV-2001 (first entry)
 DT
 XX Amino acid sequence of cancer testis tumour antigen NY-ESO-1.
 DE
 XX Cancer testis tumour antigen; NY-ESO-1; LAGE-2; human leukocyte antigen;
 KW

KW HLA; HLA binding peptide; major histocompatibility complex; MHC; tumour;
 KW cancer; testis tumour.
 XX
 XX Homo sapiens.
 XX
 PN WO200162917-A1.
 XX
 PD 30-AUG-2001.
 XX
 XX 22-JAN-2001; 2001WO-US002126.
 XX
 XX 22-FEB-2000; 2000US-00510635.
 PR
 XX (LUDW-) LUDWIG INST CANCER RES.
 XX
 XX Lethe B, Boon-Falleur T;
 XX
 XX WPI; 2001-550091/61.
 DR N-PSDB; AAH75118.
 DR
 XX Genomic sequences of tumor associated antigen EY-ESO-1 (LAGE-2) useful
 PT for diagnosing testicular tumors.
 PT
 XX Example 5; Fig 3; 50pp; English.
 XX
 XX The present sequence represents cancer testis tumour antigen NY-ESO-1
 CC (also called LAGE-2). NY-ESO-1 is a molecule that is processed to at
 CC least one human leukocyte antigen (HLA) binding peptide, which binds to
 CC Class I and Class II major histocompatibility complex (MHC). NY-ESO-1 is
 CC expressed in tumour mRNA and in testis, but not normal colon, kidney,
 CC liver or brain tissue. The presence or level of expression of NY-ESO-1
 CC may be assayed for the diagnosis of cancer, especially testis tumours
 XX
 XX Sequence 180 AA;
 SQ
 Query Match 100.0%; Score 959; DB 4; Length 180;
 Best Local Similarity 100.0%; Pred. No. 5,2e-79;
 Matches 180; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MQAEGRTGSGTGDADPGGPGIPDGGNAGGPGGAGATGGRGPRGAGAAASGPGGGA 60
 DB 1 MQAEGRTGSGTGDADPGGPGIPDGGNAGGPGGAGATGGRGPRGAGAAASGPGGGA 60
 QY 61 PRGPHGGAASGLNGCCRCGARGPESRLLEFYLLAMPFATPMEALARRSLAQDAPPLVPVG 120
 DB 61 PRGPHGGAASGLNGCCRCGARGPESRLLEFYLLAMPFATPMEALARRSLAQDAPPLVPVG 120
 QY 121 VLLKEFTVSGNLTIRLTAAADHRQLQLSISSCLQLSLMWITQCFLPVFLAQPSPGQRR 180
 DB 121 VLLKEFTVSGNLTIRLTAAADHRQLQLSISSCLQLSLMWITQCFLPVFLAQPSPGQRR 180
 RESULT 9
 AAU01535
 ID AAU01535 standard; protein; 180 AA.
 AC AAU01535;
 XX
 XX 18-JUL-2001 (first entry)
 XX
 XX Human NY-ESO-1 tumour rejection antigen precursor protein.
 XX
 XX NY-ESO-1; human; tumour rejection antigen precursor; SX-2; MHC Class II;
 KW major histocompatibility complex; helper T cell; HLA-DR; cancer;
 KW human leukocyte antigen-determining region; disease progression;
 KW disease regression; disease onset; body tissue; body fluid; enzyme label;
 KW radioactive label; monoclonal antibody.
 XX
 XX Homo sapiens.
 OS
 XX
 XX Key Location/Qualifiers
 FH Modified-site 7
 FT Modified-site /note= "Myristoylated"
 FT

FT Modified-site 9 /note= "Myristoylated"
 FT Modified-site 11 /note= "Phosphorylated"
 FT Modified-site 98 /note= "Phosphorylated"
 FT Modified-site 134 /note= "Phosphorylated"
 FT Modified-site 138 /note= "Phosphorylated"
 FT Modified-site /note= "Phosphorylated"
 XX
 PN WO200123560-A2.
 XX
 XX 05-APR-2001.
 XX
 XX 26-SEP-2000; 2000WO-US026411.
 XX
 XX 29-SEP-1999; 99US-00408036.
 PR
 XX (LUDW-) LUDWIG INST CANCER RES.
 PA
 XX Tureci O, Sahin U, Pfreundschuh M;
 PI
 XX WPI; 2001-266156/27.
 DR N-PSDB; AAS02254.
 DR
 XX
 XX Polypeptides binding to major histocompatibility complex class II human
 PT leukocyte antigen-determining region molecule having amino acid sequence
 PT found in tumor rejection antigen precursor used for stimulating
 PT proliferation of helper T cells.
 XX
 XX Claim 4; Fig 3; 62pp; English.
 XX
 XX The sequence represents a human NY-ESO-1 tumour rejection antigen
 CC precursor. NY-ESO-1 and SX-2 polypeptides, or fragments of, bind to
 CC major histocompatibility complex (MHC) Class II molecules such as human
 CC leukocyte antigen-determining region (HLA-DR) molecules and stimulate
 CC proliferation of helper T cells. The peptides can be administered to an
 CC HLA-DR positive subject in order to stimulate the helper T cells. An MHC
 CC Class II HLA-DR-NY-ESO-1/SX-2 complex expressed on the surface of a cell
 CC or present in free form is useful for this stimulation. The nucleic acid
 CC is useful for screening for a cancerous condition, which involves
 CC contacting a subject sample to a cell line transfected with the
 CC immunoreactive cell (helper T cell), where interaction is indicative of
 CC cancer. In addition, a sample from a patient (for example, a body fluid
 CC or tissue) can be monitored for the amount of the complex present in the
 CC bloodstream. This is useful for determining regression, progression or
 CC onset of a cancerous condition. The method involves contacting the sample
 CC with a radioactive labelled or enzyme labelled monoclonal antibody which
 CC specifically binds with the complex
 XX
 XX Sequence 180 AA;
 SQ
 Query Match 100.0%; Score 959; DB 4; Length 180;
 Best Local Similarity 100.0%; Pred. No. 5,2e-79;
 Matches 180; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MQAEGRTGSGTGDADPGGPGIPDGGNAGGPGGAGATGGRGPRGAGAAASGPGGGA 60
 DB 1 MQAEGRTGSGTGDADPGGPGIPDGGNAGGPGGAGATGGRGPRGAGAAASGPGGGA 60
 QY 61 PRGPHGGAASGLNGCCRCGARGPESRLLEFYLLAMPFATPMEALARRSLAQDAPPLVPVG 120
 DB 61 PRGPHGGAASGLNGCCRCGARGPESRLLEFYLLAMPFATPMEALARRSLAQDAPPLVPVG 120
 QY 121 VLLKEFTVSGNLTIRLTAAADHRQLQLSISSCLQLSLMWITQCFLPVFLAQPSPGQRR 180
 DB 121 VLLKEFTVSGNLTIRLTAAADHRQLQLSISSCLQLSLMWITQCFLPVFLAQPSPGQRR 180
 RESULT 10
 AAU07714
 ID AAU07714 standard; protein; 180 AA.

```
XX AC AAE07714;
XX XX
XX DT 06-NOV-2001 (first entry)
XX XX
XX DE Human NY ESO-1 protein.
XX XX
XX KW Human; major histocompatibility complex; MHC; vaccine; metastasis;
XX KW class II restricted T cell epitope; MHC-II epitope; cancer antigen;
XX KW NY ESO-1 protein; CD4+ T lymphocyte; human leucocyte antigen; HLA;
XX KW tumour-specific humoral-mediated immunity; cancer; cytostatic;
XX KW immunotherapy.
XX XX
XX OS Homo sapiens.
XX XX
XX XX Key Location/Qualifiers
XX FT MISC-difference 45..47
XX FT /note= "Encoded by CCGGGGCG"
XX PN WO200155393-A2.
XX XX
XX XX 02-AUG-2001.
XX XX
XX XX 26-JAN-2001; 2001WO-US002765.
XX XX
XX XX 28-JAN-2000; 2000US-0179004P.
XX PR 29-SEP-2000; 2000US-0237107P.
XX XX
XX XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX PA
XX XX Wang R, Rosenberg SA, Zeng G;
XX PI WPI; 2001-496851/54.
XX XX
XX DR N-PSDB; AAD14179, AAD14180.
XX XX
XX XX New NY-ESO cancer peptide or MHC class II restricted T cell epitopes,
XX PT useful as immunogen and vaccine for inhibiting cancer in a mammal or as
XX PT protection from metastasis.
XX XX
XX XX Example 1; Fig 1; 134pp; English.
XX XX
XX CC The invention relates to the identification and isolation of major
XX CC histocompatibility (MHC) class II restricted T cell epitope (MHC-II
XX CC epitope) derived from the cancer antigen, NY ESO-1. The MHC-II epitopes
XX CC from NY ESO-1 are recognised by CD4+ T lymphocytes in an human leucocyte
XX CC antigen (HLA) class II restricted manner, in particular HLA-DR or HLA-DP
XX CC restricted. The products of the gene are promising candidates for
XX CC immunotherapeutic strategies for the prevention, treatment and diagnosis
XX CC of patients with cancer. The cancer epitopes are useful as immunogen and
XX CC vaccine to inhibit or to prevent cancer in a mammal by eliciting CD4+ T
XX CC lymphocytes resulting in protection of the recipient from development of
XX CC cancer and protection from metastasis, or by inhibiting the growth of
XX CC cells expressing the NY-ESO-1 gene product. The cancer peptides are also
XX CC useful as diagnostic agent to detect the presence of cancer, to enhance
XX CC the generation of antibody and/or CD8+ T cell responses against any given
XX CC target antigen and/or hapten and to induce tumour-specific humoral-
XX CC mediated immunity against cancer. The present sequence is human NY ESO-1
XX CC protein
XX XX
XX SQ Sequence 180 AA;
Query Match 100.0%; Score 959; DB 4; Length 180;
Best Local Similarity 100.0%; Pred. No. 5.2e-79;
Matches 180; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MQAEGRTGSGTDADGPGGPGIIPDGGNAGGPGAGATGGRGPRGAGAAASGPGGA 60
DB 1 MQAEGRTGSGTDADGPGGPGIIPDGGNAGGPGAGATGGRGPRGAGAAASGPGGA 60
QY 61 PRGPHGGAAGLNGCCRGARGPESLLEFYLAMPATPMEALRRSLAQDAPPLPVPG 120
DB 61 PRGPHGGAAGLNGCCRGARGPESLLEFYLAMPATPMEALRRSLAQDAPPLPVPG 120
```

```
QY 121 VLLKEFTVSGNLTIRLTAAADHRQLQLSISSCLQLSLMLWITQCFLPVFLAQPSPGQR 180
DB 121 VLLKEFTVSGNLTIRLTAAADHRQLQLSISSCLQLSLMLWITQCFLPVFLAQPSPGQR 180
RESULT 11
AAU84818
ID AAU84818 standard; protein; 180 AA.
XX AC AAU84818;
XX XX
XX DT 08-MAY-2002 (first entry)
XX XX
XX DE Human NYNSO1a consensus sequence.
XX XX
XX KW Savine; vaccine; cancer; viral infection; HIV; hepatitis C virus;
XX KW viral infection; human immunodeficiency virus; melanoma;
XX KW bacterial infection; Salmonella; Legionella; parasitic infection;
XX KW Trypanosoma; Toxoplasma; Giardia.
XX XX
XX OS Homo sapiens.
XX XX
XX PN WO200190197-A1.
XX XX
XX PD 29-NOV-2001.
XX XX
XX PF 25-MAY-2001; 2001WO-AU000622.
XX XX
XX PR 26-MAY-2000; 2000AU-00007761.
XX XX
XX XX (AUSU ) UNIV AUSTRALIAN NAT.
XX XX
XX XX Thomson SA, Ramshaw IA;
XX XX
XX DR WPI; 2002-147575/19.
XX XX
XX PT New synthetic polypeptides having several different segments of at least
XX PT one parent polypeptide linked together differently compared to the
XX PT linkage in the parent polypeptide, for inducing immune response against a
XX PT pathogen or cancer.
XX XX
XX PS Example 3; Fig 27; 364pp; English.
XX XX
XX CC The invention relates to a new synthetic polypeptide (I) comprising
XX CC several different segments of at least one parent polypeptide linked
XX CC together in a different relationship relative to their linkage in the
XX CC parent polypeptide to impede, abrogate or otherwise alter at least one
XX CC function associated with the parent polypeptide and for inducing an
XX CC immune response against a pathogen or cancer. Also included are a
XX CC synthetic polynucleotide encoding and a computer system for designing the
XX CC synthetic polypeptides. The synthetic polypeptides and polynucleotides
XX CC are referred to as a Savine. The synthetic polypeptide is useful for
XX CC modulating immune responses preferably directed against a pathogen or a
XX CC cancer, (e.g., cancers of the lung, breast, ovary, cervix, colon, head
XX CC and neck, pancreas, prostate, stomach, bladder, kidney, bone liver,
XX CC oesophagus, brain, testicle, uterus), as potentiating agents.
XX CC Compositions comprising the polypeptide may be used in the treatment or
XX CC prophylaxis against viral (such as infections caused by HIV (human
XX CC immunodeficiency virus), hepatitis, influenza, Japanese encephalitis
XX CC virus, Epstein-Barr virus and respiratory syncytial virus), bacterial
XX CC (e.g., infections caused by Neisseria, Meningococcus, Haemophilus,
XX CC Salmonella, Streptococcus, Legionella and Mycobacterium or parasitic
XX CC (e.g., infections caused by Plasmodium, Schistosoma, Leishmania,
XX CC Trypanosoma, Toxoplasma and Giardia) infections. The present sequence is
XX CC a consensus sequence for a parent protein used to design a savine of the
XX CC invention
XX XX
XX SQ Sequence 180 AA;
Query Match 100.0%; Score 959; DB 5; Length 180;
Best Local Similarity 100.0%; Pred. No. 5.2e-79;
Matches 180; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

QY 1 MQAEGRGTSSTGDADPGGPGIPDPGGNAGGPGGAGATGGRGPRGAGAAASGPGGGA 60
 |||||
 Db 1 MQAEGRGTSSTGDADPGGPGIPDPGGNAGGPGGAGATGGRGPRGAGAAASGPGGGA 60
 |||||
 QY 61 PRGPHGGAASGLNGCCRCGARGPESRLLEFYLLAMPFATPMEAEARRSLAQDAPPLVPVG 120
 |||||
 Db 61 PRGPHGGAASGLNGCCRCGARGPESRLLEFYLLAMPFATPMEAEARRSLAQDAPPLVPVG 120
 |||||
 QY 121 VLLKEFTVSGNLTIRLTAAHRLQLSISCLQLSLLMWITQCFPLVFLAOPPSGQRR 180
 |||||
 Db 121 VLLKEFTVSGNLTIRLTAAHRLQLSISCLQLSLLMWITQCFPLVFLAOPPSGQRR 180
 |||||
 RESULT 12
 AAU11543
 ID AAU11543 standard; protein; 180 AA.
 XX
 AC AAU11543;
 XX
 DT 12-MAR-2002 (first entry)
 XX
 DE Human tumour associated antigen NY-ESO.
 XX
 KW Human; tumour associated antigen; NY-ESO; human leukocyte antigen;
 KW major histocompatibility complex; MHC; HLA-A2.2; vaccine; cancer; HIV;
 KW human immunodeficiency virus infection; cytostatic; virucide;
 KW housekeeping epitope; adoptive immunotherapy; neoplastic disease;
 KW viral disease; hepatitis virus; papilloma virus; tumour; leukaemia;
 KW lymphoma; breast cancer; prostate cancer; lung cancer;
 KW parasitic infection; Chlamydia; Trypanosoma; Toxoplasma.
 XX
 OS Homo sapiens.
 XX
 PN WO200182963-A2.
 XX
 PD 08-NOV-2001.
 XX
 PF 27-APR-2001; 2001WO-US013806.
 XX
 PR 28-APR-2000; 2000US-00560465.
 PR 28-APR-2000; 2000US-00561074.
 PR 28-APR-2000; 2000US-00561571.
 PR 28-APR-2000; 2000US-00561572.
 XX
 XX (CTLI-) CTL IMMUNOTHERAPIES CORP.
 PA
 XX Simard JUL, Diamond DC, Lei X;
 XX
 XX WPI; 2002-066492/09.
 XX
 XX Novel vaccine useful for treating neoplastic and viral diseases,
 PT comprises a first housekeeping epitope derived from a first antigen
 PT associated with a first target cell.
 XX
 XX Example 23; Fig 17; 131pp; English.
 XX
 XX The invention relates to a vaccine comprising a first housekeeping
 CC epitope derived from a first antigen associated with a first target cell.
 CC Also included are an isolated T cell expressing a T cell receptor
 CC specific for a major histocompatibility complex (MHC)-peptide complex
 CC comprising a first housekeeping epitope which is derived from a first
 CC antigen associated with a first target cell, selecting an epitope (or
 CC peptide sequence) from a population of peptide fragments of an antigen
 CC associated with a target in a host, where the fragments have a known or
 CC predicted affinity for a MHC receptor peptide binding cleft of the host,
 CC where the epitope selected corresponds to a product of proteolytic
 CC cleavage of the antigen in a cell of the host and a nucleic acid
 CC construct comprising a first coding region, where the first coding region
 CC comprises a first sequence encoding at least a first polypeptide, where
 CC the first polypeptide comprises a first housekeeping epitope derived from
 CC a first antigen associated with a first target cell; The epitopes,
 CC peptides, vaccines and nucleic acids are useful in the manufacture of a
 CC medicament for use in adoptive immunotherapy and for prevention and

CC treatment of neoplastic and viral diseases (e.g. human immunodeficiency
 CC virus, HIV, infection, hepatitis virus and papilloma virus), cancers
 CC (e.g. tumours, leukaemia, lymphoma, breast cancer, prostate cancer and
 CC lung cancer), infection of cells by intracellular parasites (e.g.
 CC Chlamydia, Trypanosoma and Toxoplasma) and many other examples given in
 CC the specification. The invention permits the vaccine designer to ignore
 CC peptides that, despite predicted high binding affinity for MHC, will
 CC never be useful because they cannot be presented by target cells. The
 CC invention provides a major advance in vaccine design, one that combines
 CC the power of antigen sequence analysis with the fundamental realities of
 CC immunology. The invention allows for the simple and effective selection
 CC of meaningful epitopes for creation of MHC class I or Class II vaccines
 CC using any polypeptide sequence corresponding to a desired target. The
 CC present sequence is an HLA-A2.1 (human leukocyte antigen) presenting
 CC target cell protein from which epitopes of the invention may be derived,
 CC NY-ESO (a tumour associated antigen)
 XX
 SQ Sequence 180 AA;
 Query Match 100.0%; Score 959; DB 5; Length 180;
 Best Local Similarity 100.0%; Pred. No. 5.2e-79;
 Matches 180; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MQAEGRGTSSTGDADPGGPGIPDPGGNAGGPGGAGATGGRGPRGAGAAASGPGGGA 60
 |||||
 Db 1 MQAEGRGTSSTGDADPGGPGIPDPGGNAGGPGGAGATGGRGPRGAGAAASGPGGGA 60
 |||||
 QY 61 PRGPHGGAASGLNGCCRCGARGPESRLLEFYLLAMPFATPMEAEARRSLAQDAPPLVPVG 120
 |||||
 Db 61 PRGPHGGAASGLNGCCRCGARGPESRLLEFYLLAMPFATPMEAEARRSLAQDAPPLVPVG 120
 |||||
 QY 121 VLLKEFTVSGNLTIRLTAAHRLQLSISCLQLSLLMWITQCFPLVFLAOPPSGQRR 180
 |||||
 Db 121 VLLKEFTVSGNLTIRLTAAHRLQLSISCLQLSLLMWITQCFPLVFLAOPPSGQRR 180
 |||||
 RESULT 13
 ABR58672
 ID ABR58672 standard; protein; 180 AA.
 XX
 AC ABR58672;
 XX
 XX 09-JUL-2003 (first entry)
 XX
 XX Human cancer related protein SEQ ID NO:329.
 DE
 XX Human; cancer; diagnosis; screening; modulator; leukaemia; ischaemia;
 KW heart disease; atherosclerosis; endometriosis.
 KW
 XX Homo sapiens.
 OS
 XX WO2003025138-A2.
 PN
 XX 27-MAR-2003.
 PD
 XX 17-SEP-2002; 2002WO-US029560.
 PF
 XX 17-SEP-2001; 2001US-0323469P.
 PR 20-SEP-2001; 2001US-0323887P.
 PR 13-NOV-2001; 2001US-0350666P.
 PR 08-FEB-2002; 2002US-0355145P.
 PR 08-FEB-2002; 2002US-0355257P.
 PR 12-APR-2002; 2002US-0372246P.
 XX
 XX (EOSB-) EOS BIOTECHNOLOGY INC.
 PA
 XX Afar D, Aziz N, Gish KC, Hevezi PA, Mack DH, Wilson KE;
 PI Zlotnik A;
 PI
 XX WPI; 2003-354600/33.
 DR N-PSDB; ACC72823.
 DR
 XX New genes that are up-regulated or down-regulated in cancers, useful as
 PT

PT markers for diagnosing e.g. cancer, ischemia or heart diseases, or as
XX therapeutic targets for screening drugs for treating these diseases.

PS Claim 12; Page 757-758; 767pp; English.

XX The present invention describes an isolated nucleic acid molecule, which
CC comprises the sequence of any of the genes that are up-regulated or down-
CC regulated in specific cancers (e.g. about 1031 genes up-regulated in
CC acute lymphocytic leukemia). ACC72641 to ACC72860 represent cancer
CC related gene nucleotide sequences which encode the proteins given in
CC ABR59521 to ABR58709. Also described: (1) determining the presence or
CC absence of a pathological cell in a patient; (2) an expression vector
CC comprising a nucleic acid molecule described above; (3) a host cell
CC comprising the vector; (4) an isolated polypeptide, which is encoded by
CC the nucleic acid; (5) an antibody that specifically binds the polypeptide
CC of (4); (6) specifically targeting a compound to a pathological cell in a
CC patient by administering to the patient the antibody above; and (7) a
CC drug screening assay. The nucleic acid is useful as diagnostic markers or
CC therapeutic targets. In particular, the nucleic acid is useful for
CC diagnosing a pathology, e.g. cancer (e.g. cancer of the bone marrow,
CC bladder, brain, breast, cervix, colon/rectum, kidney, lung, ovary,
CC pancreas, prostate, skin and uterus), wounds, ischaemia, heart diseases,
CC atherosclerosis and endometriosis. The nucleic acid is also useful in
CC drug screening, particularly for identifying agents for treating these
CC pathologies

XX SQ Sequence 180 AA;

Query Match 100.0%; Score 959; DB 6; Length 180;
Best Local Similarity 100.0%; Pred. No. 5.2e-79;
Matches 180; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MQAEGRTGSGTGDADGPGGPGIPDGGNAGGPGGAGATGGRGAGAAASGPGGGA 60
DB 1 MQAEGRTGSGTGDADGPGGPGIPDGGNAGGPGGAGATGGRGAGAAASGPGGGA 60
QY 61 PRPHGGAASGLNGCCRCGARGPESRLLEFYLLAMPFATPMEALARRSLAQDAPPLVPVG 120
DB 61 PRPHGGAASGLNGCCRCGARGPESRLLEFYLLAMPFATPMEALARRSLAQDAPPLVPVG 120
QY 121 VLLKEFTVSGNLTIRLTAADHRQLQLSISSCLQLSLMWITQCFPLVFLAQPSPGQRR 180
DB 121 VLLKEFTVSGNLTIRLTAADHRQLQLSISSCLQLSLMWITQCFPLVFLAQPSPGQRR 180

RESULT 14

ABR48210
ID ABR48210 standard; protein; 180 AA.

XX AC ABR48210;

XX DT 12-JUN-2003 (first entry)

XX DE Human bladder cancer associated protein sequence SEQ ID NO:139.

XX KW Human; bladder cancer; cytostatic; gene therapy; vaccine.

XX OS Homo sapiens.

XX PN WO2003003906-A2.

XX PD 16-JAN-2003.

XX PF 03-JUL-2002; 2002WO-US021338.

XX PR 03-JUL-2001; 2001US-0302814P.

XX PR 03-AUG-2001; 2001US-0310099P.

XX PR 08-NOV-2001; 2001US-0343705P.

XX PR 13-NOV-2001; 2001US-0350666P.

XX PR 12-APR-2002; 2002US-0372246P.

XX PA (BOSB-) EOS BIOTECHNOLOGY INC.

XX

PI Mack DH, Aziz N;

XX WPI; 2003-201532/19.

DR N-PSDB; ACC51024.

XX Detecting a bladder cancer-associated transcript in a cell from a
PT patient, comprises contacting a biological sample from the patient with a
PT bladder cancer-associated polynucleotide or antibody.

XX PS Claim 10; Page 278; 307pp; English.

XX The present invention describes a method for detecting a bladder cancer-
CC associated transcript in a cell from a patient. The method comprises
CC contacting a biological sample from the patient with a polynucleotide
CC that selectively hybridizes to a sequence that is 80 % identical to a
CC table of sequences (see ACC50951 to ACC51059). ACC50951 to ACC51059
CC encode the human bladder cancer-associated proteins given in ABR48146 to
CC ABR48242). Bladder cancer-associated sequences from the present invention
CC have cytostatic activities, and can be used in antisense gene therapy and
CC in vaccine production. The method can be used for detecting a bladder
CC cancer-associated transcript in a cell from a patient. The method is
CC useful in diagnosing or treating bladder cancer and in screening for
CC compounds that modulate bladder cancer, such as hormones or antibodies.
CC The nucleic acid molecules from the present invention may be used in
CC various screening and diagnostic methods, and for gene therapy, vaccine
CC and/or antisense/inhibition applications

XX SQ Sequence 180 AA;

Query Match 100.0%; Score 959; DB 6; Length 180;
Best Local Similarity 100.0%; Pred. No. 5.2e-79;
Matches 180; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MQAEGRTGSGTGDADGPGGPGIPDGGNAGGPGGAGATGGRGAGAAASGPGGGA 60
DB 1 MQAEGRTGSGTGDADGPGGPGIPDGGNAGGPGGAGATGGRGAGAAASGPGGGA 60
QY 61 PRPHGGAASGLNGCCRCGARGPESRLLEFYLLAMPFATPMEALARRSLAQDAPPLVPVG 120
DB 61 PRPHGGAASGLNGCCRCGARGPESRLLEFYLLAMPFATPMEALARRSLAQDAPPLVPVG 120
QY 121 VLLKEFTVSGNLTIRLTAADHRQLQLSISSCLQLSLMWITQCFPLVFLAQPSPGQRR 180
DB 121 VLLKEFTVSGNLTIRLTAADHRQLQLSISSCLQLSLMWITQCFPLVFLAQPSPGQRR 180

RESULT 15

ABU56508

ID ABU56508 standard; protein; 180 AA.

XX AC ABU56508;

XX DT 02-APR-2003 (first entry)

XX DE Lung cancer-associated polypeptide #101.

XX KW Lung cancer-associated polypeptide; cytostatic; emphysema;

XX KW antinflammatory; antiasthmatic; non-small cell lung cancer; atelectasis;

XX KW small cell lung cancer; benign lesion; precancerous lesion; bronchitis;

XX KW chronic obstructive pulmonary disease; hypersensitivity pneumonitis;

XX KW interstitial pulmonary fibrosis; fibrosis; asthma; bronchiectasis.

XX OS Unidentified.

XX PN WO200286443-A2.

XX PD 31-OCT-2002.

XX PF 18-APR-2002; 2002WO-US012476.

XX PR 18-APR-2001; 2001US-0284770P.

XX PR 10-MAY-2001; 2001US-0290492P.

XX PR 09-NOV-2001; 2001US-0339245P.

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OM protein - protein search, using sw model

Run on: September 11, 2005, 01:28:54 ; Search time 50.5714 Seconds
(without alignments)
342.466 Million cell updates/sec

Title: US-09-529-206E-4
Perfect score: 959
Sequence: 1 MQAEGRTGSGTDADPGG.....WITQCLPVLQAQPSGGQR 180

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	174.5	18.2	627	T35608	polyketide hydroxy
2	155.5	16.2	145	T08435	la costa protein -
3	155.5	16.2	641	Q0831	nuclear antigen EB
4	153	16.0	1079	E70807	hypothetical glyci
5	152.5	15.9	779	CGB01S	collagen alpha 1(I
6	151.5	15.8	1464	CGHUIS	collagen alpha 1(I
7	151	15.7	1489	D70807	hypothetical glyci
8	151	15.7	1901	F70806	hypothetical glyci
9	150.5	15.7	530	T32812	hypothetical prote
10	149.5	15.6	615	H70589	hypothetical glyci
11	149.5	15.6	1215	T32734	myosin-IA - Acanth
12	149	15.5	297	T27525	hypothetical prote
13	149	15.5	299	T20605	hypothetical prote
14	148.5	15.5	252	S01821	glycine-rich prote
15	148.5	15.5	1042	CGCHIS	collagen alpha 1(I
16	147.5	15.4	473	T50629	collagen - chicken
17	147	15.3	296	T21070	hypothetical prote
18	147	15.3	440	F85584	probable tail comp
19	147	15.3	1381	E70806	hypothetical glyci
20	146.5	15.3	290	T24590	hypothetical prote
21	146.5	15.3	1806	CGHULE	collagen alpha 1(X
22	146	15.2	338	KNMU	glycine-rich cell
23	146	15.2	853	A70896	hypothetical glyci
24	146	15.2	1880	T18531	tractin - medicina
25	145.5	15.2	228	S19312	glycine-rich prote
26	145.5	15.2	482	B31795	collagen alpha 1(X
27	145.5	15.2	1306	A70934	hypothetical glyci
28	145	15.1	741	G70917	hypothetical glyci
29	145	15.1	1329	E70917	hypothetical glyci

30	144.5	15.1	290	2	T24586	hypothetical prote
31	144.5	15.1	301	2	B31219	collagen 2 - Caeno
32	144.5	15.1	330	2	T26004	hypothetical prote
33	144.5	15.1	438	2	D90734	probable tail fibe
34	144.5	15.1	1147	1	MWAXIB	myosin heavy chain
35	144	15.0	667	2	A70893	hypothetical glyci
36	143.5	15.0	310	2	I50696	collagen alpha 1(I
37	143.5	15.0	314	2	T32247	hypothetical prote
38	143.5	15.0	714	2	A70807	hypothetical glyci
39	143.5	15.0	886	2	I50694	collagen alpha 1(I
40	143.5	15.0	1049	1	CGB07S	collagen alpha 1(I
41	143	14.9	323	2	T19142	hypothetical prote
42	143	14.9	437	2	H90854	probable tail fibe
43	143	14.9	439	2	C90769	probable tail fibe
44	143	14.9	1660	2	A70869	hypothetical glyci
45	142.5	14.9	244	2	T49893	glycine-rich prote

ALIGNMENTS

RESULT 1

T35608 polyketide hydroxylase - Streptomyces coelicolor

C;Species: Streptomyces coelicolor

C;Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 09-Jul-2004

C;Accession: T35608

R;Seeger, K.J.; Harris, D.; James, K.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.

submitted to the EMBL Data Library, June 1999

A;Reference number: Z21584

A;Accession: T35608

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-627 <SEE>

A;Cross-references: UNIPROT:P42534; EMBL:AL079356; PIDN:CAB45603.1; GSPDB:GN00070; SCORE

A;Experimental source: strain A3(2)

C;Genetics:

A;Gene: SCOEDB:SC6G9.12c

C;Superfamily: tetracycline 6-hydroxylase

Query Match 18.2%; Score 174.5; DB 2; Length 627;

Best Local Similarity 42.7%; Pred. No. 5e-06;

Matches 47; Conservative 4; Mismatches 28; Indels 31; Gaps 6;

QY 5 GRGTGSGTDADPGGPGIPDGGNAGGPGAGATGG-RGPRGAGAAASGPGGAPRG 63

Db 409 GRGTGCG-FCGPGCGGLGCGPGCGG-TGGPGGPGGPGDGRGAGAGFCGGGPGG----G 462

QY 64 PHGGAASGLNGCCRCGARGPESRLLEFFYLAMPF-----ATPMEAE 103

Db 463 PGGG-----GPGRGILNVALGYRYPGAVGVGADPATPVWPE 498

RESULT 2

T08435

la costa protein - fruit fly (Drosophila melanogaster)

C;Species: Drosophila melanogaster

C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004

C;Accession: T08435

R;Maleszka, R.; de Couet, H.G.; Miklos, G.L.

Proc. Natl. Acad. Sci. U.S.A. 95, 3731-3736, 1998

A;Title: Data transferability from model organisms to human beings: insights from the f

A;Reference number: Z16415; MUID:98188272; PMID:9520435

A;Accession: T08435

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-145 <MAL>

A;Cross-references: UNIPROT:O61351; EMBL:AF017777; NID:G3004652; PIDN:AAC28405.1; PID:G

A;Experimental source: strain Cantons

C;Genetics:

A;Gene: lcs

A;Cross-references: FlyBase:FlyBase:FBgn0024251

Db 140 GAGAAGAPGAGGPGGAGLWNGGPGGAGGSGGTGAGGAGGWLFGVGGAGGAGG 199
QY 49 GAARASGPG---GGAPRPHGGAASGLNG 74
Db 200 GTGAGGPGGLWNGGAGGAGGAGGAGGTGG 229

RESULT 8

F70806
hypothetical glycine-rich protein Rv3508 - Mycobacterium tuberculosis (strain H37RV)
C:Species: Mycobacterium tuberculosis
C>Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004
C:Accession: F70806
R: Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
A: Authors: Squires, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A: Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome
A: Reference number: A70500; MUID: 98295987; PMID: 9634230
A: Accession: F70806
A: Status: preliminary; nucleic acid sequence not shown; translation not shown
A: Molecule type: DNA
A: Residues: 1-1901 <COL>
A: Cross-references: UNIPROT: O53553; GB: AL022022; GB: AL123456; NID: g3261554; PIDN: CAA1774
A: Experimental source: strain H37RV
C: Genetics:
A: Gene: Rv3508
C: Superfamily: collagen alpha 1(IV) chain

Query Match 15.7%; Score 151; DB 2; Length 1901;
Best Local Similarity 41.1%; Pred. No. 0.00082;
Matches 37; Conservative 2; Mismatches 31; Indels 20; Gaps 3;
QY 5 GRTGGSTGADGPGGP-----GIPDPCGNAGGPGEA-----GATCGRPRGA 48
Db 140 GAGAAGAPGAGGPGGAGLWNGGPGGAGGSGGTGAGGAGGWLFGVGGAGGAGG 199
QY 49 GAARASGPG---GGAPRPHGGAASGLNG 74
Db 200 GTGAGGPGGLWNGGAGGAGGAGGAGGTGG 229

RESULT 9

T32812
hypothetical protein H17B01.2 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
C:Accession: T32812
R: Gattung, S.; Maggi, L.
submitted to the EMBL Data Library, December 1997
A: Description: The sequence of C. elegans cosmid H17B01.
A: Reference number: Z21227
A: Accession: T32812
A: Status: preliminary; translated from GB/EMBL/DDBJ
A: Molecule type: DNA
A: Residues: 1-530 <GAT>
A: Cross-references: UNIPROT: O61209; EMBL: AF040646; PIDN: AAB94986.1; GSPDB: GNO00020; CESP:
A: Experimental source: strain Bristol N2; clone H17B01
C: Genetics:
A: Gene: CESP:H17B01.2
A: Map position: 2
A: Introns: 42/3; 58/1; 173/3; 268/2; 308/2; 340/1; 364/2; 387/3

Query Match 15.7%; Score 150.5; DB 2; Length 530;
Best Local Similarity 32.3%; Pred. No. 0.00028;
Matches 51; Conservative 9; Mismatches 65; Indels 33; Gaps 8;
QY 5 GRTGGSTGADGPGGPGIPDPCGNAGGPGGAGATGGRG-PRGAGARASGPGGAPRG 63
Db 96 GLGTPGPGNPGGGLGTLTGGP-GTTPGGPNPGGLGPNPGGPGTGGPGTGGPGPHG 154

QY 64 PHGGAASGL---NG-----CCRC-----GARGPESRLLEFYLAMPF-----ATPMEAEAR 106
Db 155 TAGGTYYIIVQNGQRVIVNCATRCCLCCGRNITYSVVTDSPVVPVLAVTGTB----- 207
QY 107 RSLAQDAPLPV-----PGVLLKEFTVSGNLTIRLT 138
Db 208 -SIVTVTPSPSVTPGCRFGSTPPATFPFGSVSTVRYT 244

RESULT 10

H70589
hypothetical glycine-rich protein Rv2853 - Mycobacterium tuberculosis (strain H37RV)
C:Species: Mycobacterium tuberculosis
C>Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 31-Mar-2003
C:Accession: H70589
R: Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
A: Authors: Squires, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A: Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome
A: Reference number: A70500; MUID: 98295987; PMID: 9634230
A: Accession: H70589
A: Status: preliminary; nucleic acid sequence not shown; translation not shown
A: Molecule type: DNA
A: Residues: 1-615 <COL>
A: Cross-references: GB: Z95207; GB: AL123456; NID: g3261745; PIDN: CAB08453.1; PID: e315182;
A: Experimental source: strain H37RV
C: Genetics:
A: Gene: Rv2853
C: Superfamily: uncharacterized glycine-rich protein, PE motif containing

Query Match 15.6%; Score 149.5; DB 2; Length 615;
Best Local Similarity 49.3%; Pred. No. 0.00039;
Matches 35; Conservative 5; Mismatches 26; Indels 5; Gaps 3;
QY 7 GTGGSTGADGPGGPGIPDPCGNAGG--PGAGATGGRGPRGA-GAARASGPGGAPRG 63
Db 532 GTGGNGDGGAGAPGL--GGAGGAGGWLIGSGSTGGGAGGAGGAGGAGGAGG 589
QY 64 PHGGAASGLNG 74
Db 590 GHGDTTSGKNG 600

RESULT 11

T32734
myosin-IA - Acanthamoeba castellanii
C:Species: Acanthamoeba castellanii
C>Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
C:Accession: T32734
R: Lee, W.L.; Ostap, E.M.; Zot, H.G.; Pollard, T.D.
submitted to the EMBL Data Library, August 1998
A: Description: Hydrodynamic and ligand binding properties of Acanthamoeba myosin-IA GPA.
A: Reference number: Z21216
A: Accession: T32734
A: Status: preliminary; translated from GB/EMBL/DDBJ
A: Molecule type: DNA
A: Residues: 1-1215 <LEE>
A: Cross-references: UNIPROT: O77202; EMBL: AF085185; NID: g3599477; PID: g3599478; PIDN: AAC
A: Experimental source: strain Neff
C: Genetics:
A: Gene: MIA
A: Introns: 1/3; 41/3; 72/2; 103/2; 162/3; 184/1; 217/1; 296/1; 340/3; 390/3; 447/3; 500/
C: Superfamily: protozoan myosin heavy chain IB; myosin motor domain homology; SH3 homol
F: 14-674/Domain: myosin motor domain homology <MMO>
Query Match 15.6%; Score 149.5; DB 2; Length 1215;
Best Local Similarity 41.0%; Pred. No. 0.00072;
Matches 41; Conservative 3; Mismatches 33; Indels 23; Gaps 4;
QY 5 GRGTGGS-----TGADGPG-----GFGIPDPCGNAGGPGGAGATGGRG 45

Db 931 RGDKGTGEQDRGMKGHRGFSGLQGPFGPPGAPGEQPSGASGPAG--PRGPPGSAGAA 988
Qy 71 ---GLNGC-CRCGARGPESRLLEFYLAMPPFATPMEAEIARRSLAQDAPPLPVPGLLKEF 126
Db 989 GKDGLNGLPGPIGPPGPRGTGEVGPVGPFP-----GPRGP-EGPFSGGF 1034
Qy 127 TVSG 130
Db 1035 DLDG 1038

Search completed: September 11, 2005, 01:43:52
Job time : 52.5714 secs

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OM protein - protein search, using sw model

Run on: September 11, 2005, 01:20:48 ; Search time 238.286 Seconds
(without alignments)
386.822 Million cell updates/sec

Title: US-09-529-206E-4

Perfect score: 959

Sequence: 1 MQAEGRGSGTGADGPGG.....WITQCFLPVLAQPPSGQRR 180

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Uniprot_03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	959	100.0	180	1 CTG1 HUMAN	P78358 homo sapien
2	595	62.0	210	1 CTG2 HUMAN	O75638 homo sapien
3	581	60.6	142	2 Q9NV13	Q9NV13 homo sapien
4	222	23.1	143	1 IBA2 HUMAN	Q14657 homo sapien
5	174.5	18.2	627	1 HYDL_STRCO	P42334 streptomyc
6	172.5	18.0	563	2 Q6J6N0	Q6J6N0 araneus ven
7	168.5	17.6	1002	2 Q9BIU8	Q9BIU8 argiope tri
8	167.5	17.5	922	2 O44367	O44367 mytilus edu
9	165.5	17.3	922	2 Q8MW53	Q8MW53 mytilus gal
10	162	16.9	420	2 Q6RF45	Q6RF45 arabidopsis
11	162	16.9	651	2 Q9BIU9	Q9BIU9 argiope tri
12	161	16.8	524	2 Q817U1	Q817U1 araneus ven
13	160.5	16.7	813	2 Q636W4	Q636W4 bacillus ce
14	160.5	16.7	1168	2 Q6HF99	Q6HF99 bacillus th
15	160.5	16.7	1408	2 Q7U022	Q7U022 mycobacteri
16	160.5	16.7	2249	2 Q9NHW4	Q9NHW4 nephila cla
17	160	16.7	604	2 Q9L252	Q9L252 streptomyc
18	160	16.7	871	2 Q44358	Q44358 nephila cla
19	159.5	16.6	1884	2 Q9NHW2	Q9NHW2 nephila ina
20	159	16.6	904	2 Q76271	Q76271 mytilus edu
21	158.5	16.5	678	2 Q93486	Q93486 oncorhynch
22	158.5	16.5	1458	2 Q16988	Q16988 araneus dia
23	157	16.4	410	2 Q16988	Q16988 araneus dia
24	157	16.4	626	2 Q9NHW1	Q9NHW1 nephila ina
25	156.5	16.3	1046	1 IF2_STRAW	Q82K53 streptomyc
26	155.5	16.2	145	2 Q61351	Q61351 drosophila
27	155.5	16.2	641	1 EBN1_EBV	Q61351 drosophila
28	155.5	16.2	641	2 Q777E1	Q777E1 epstein-bar
29	155	16.2	894	2 Q8MW54	Q8MW54 mytilus gal
30	155	16.2	902	2 O16161	O16161 mytilus edu
31	154.5	16.1	478	2 Q81WX2	Q81WX2 bacillus an

32	154.5	16.1	481	2	Q6HV27	Q6HV27 bacillus an
33	154.5	16.1	905	2	Q8MW55	Q8MW55 mytilus gal
34	154.5	16.1	1953	2	Q9BIT7	Q9BIT7 nephila ina
35	153	16.0	1079	2	Q6MW7	Q6MW7 mycobacteri
36	153	16.0	1449	2	Q6NZ15	Q6NZ15 brachydanio
37	153	16.0	1449	2	Q6PE19	Q6PE19 brachydanio
38	152.5	15.9	734	2	Q6IVJ4	Q6IVJ4 ciona taurus
39	152.5	15.9	779	1	CALL_BOVIN	P02453 bos taurus
40	152.5	15.9	1938	2	Q7TWCO	Q7TWCO mycobacteri
41	152	15.8	219	2	Q9D9S4	Q9D9S4 mus musculu
42	152	15.8	610	2	Q9V5V8	Q9V5V8 drosophila
43	152	15.8	1715	2	Q8VIZO	Q8VIZO mycobacteri
44	151.5	15.8	423	1	PO41_HUMAN	Q01851 homo sapien
45	151.5	15.8	809	2	O93485	O93485 oncorhynch

ALIGNMENTS

RESULT 1

ID	CTG1_HUMAN	STANDARD;	PRT;	180 AA.
AC	P78358;			
DT	15-DEC-1998 (Rel. 37, Created)			
DT	15-DEC-1998 (Rel. 37, Last sequence update)			
DT	25-OCT-2004 (Rel. 45, Last annotation update)			
DE	Cancer/testis antigen 1B (Autoimmunogenic cancer/testis antigen NY-ESO-1).			
DE	ESO-1.			
GN	Name=CTAG1B; Synonym=CTAG, CTAG1;			
OS	Homo sapiens (human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=97203161; PubMed=9050879; DOI=10.1073/pnas.94.5.1914;			
RA	Chen Y.-T., Scanlan M.J., Sahin U., Tuerci O., Gure A.O., Teang S.,			
RA	Williamson B., Stockert E., Pfreundschuh M., Old L.J.;			
RT	"A testicular antigen aberrantly expressed in human cancers detected			
RT	by autologous antibody screening."			
RL	Proc. Natl. Acad. Sci. U.S.A. 94:1914-1918(1997).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RX	TISSUE=Melanoma;			
RX	MEDLINE=98289662; PubMed=9626360;			
RA	Lethe B., Lucas S., Michaux L., de Smet C., Godelaine D., Serrano A.,			
RA	de Flaen E., Boon T.;			
RT	"LAG-1, a new gene with tumor specificity."			
RL	Int. J. Cancer 76:903-908(1998).			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=98430682; PubMed=9759882;			
RA	Wang R.-F., Johnston S.L., Zeng G., Topalian S.L.,			
RA	Schwarzenruber D.J., Rosenberg S.A.;			
RT	"A breast and melanoma-shared tumor antigen: T cell responses to			
RT	antigenic peptides translated from different open reading frames."			
RL	J. Immunol. 161:3596-3606(1998).			
CC	-!- TISSUE SPECIFICITY: Expressed in testis and ovary and in a wide			
CC	variety of cancers. Detected in uterine myometrium.			
CC	-!- SIMILARITY: Belongs to the CTAG family.			
CC	-----			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration			
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -			
CC	the European Bioinformatics Institute. There are no restrictions on its			
CC	use by non-profit institutions as long as its content is in no way			
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CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/			
CC	or send an email to license@isb-sib.ch).			
CC	-----			
DR	EMBL; U87459; AAB49693.1; -			
DR	EMBL; AU003149; CAA05908.1; -			
DR	EMBL; AF038567; AAD05202.1; -			
DR	Genew; HGNC:2491; CTAG1B.			

DR MTM; 300156; --
 KW Antigen; Transmembrane.
 FT DOMAIN 5 82 Gly-rich.
 FT TRANSMEM 156 172 Potential.
 SQ SEQUENCE 180 AA; 17992 MW; B122C5C2C8BE1569 CRC64;
 Query Match 100.0%; Score 959; DB 1; Length 180;
 Best Local Similarity 100.0%; Pred. No. 4.7e-58;
 Matches 180; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MQAEGRTGSGTGDADGPGGPGIPDGGNAGGPGAGATGGRPGAGAAASGPGGGA 60
 |||||
 Db 1 MQAEGRTGSGTGDADGPGGPGIPDGGNAGGPGAGATGGRPGAGAAASGPGGGA 60
 |||||
 QY 61 PRGPHGGAASGLNGCCRCGARGPESRLLEFYLPAMPFATPMEALARRSLAQDAPPLPVP 120
 |||||
 Db 61 PRGPHGGAASGLNGCCRCGARGPESRLLEFYLPAMPFATPMEALARRSLAQDAPPLPVP 120
 |||||
 QY 121 VLLKFTVSGNLTIRLTAAHRQLQSLSSCLQLSLLMWITQCFPLVFLAQPSPGRR 180
 |||||
 Db 121 VLLKFTVSGNLTIRLTAAHRQLQSLSSCLQLSLLMWITQCFPLVFLAQPSPGRR 180
 |||||
 RESULT 2
 CTG2_HUMAN STANDARD; PRT; 210 AA.
 ID CTG2_HUMAN
 AC 075637; 09BU80; 09UJ89; 09Y479;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Cancer/testis antigen 2 (LAGE-1 protein) (ESO-2 protein).
 GN Names=CTG2; Synonyms=ESO2, LAGE1;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 EX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORMS LAGE-1A AND LAGE-1B).
 RC TISSUE=Melanoma;
 RX MEDLINE=98289662; PubMed=9626360;
 RA Lethe B., Lucas S., Michaux L., de Smet C., Godelaine D., Serrano A.,
 de Plaen E., Boon T.;
 RT "LAGE-1, a new gene with tumor specificity.";
 RL Int. J. Cancer 76:903-908(1998).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORMS LAGE-1A AND LAGE-1B), AND VARIANTS GLN-6;
 RP GLN-89 AND ARG-138.
 RC TISSUE=Melanoma;
 RX MEDLINE=99325550; PubMed=10399963;
 RA Aarnoudse C.A., Van den Doel P.B., Heemskerk B., Schrier P.I.;
 RT "Interleukin-2-induced, melanoma-specific T cells recognize CAMEL, an
 RL Int. J. Cancer 82:442-448(1999).
 RN [3]
 RP SEQUENCE FROM N.A. (ISOFORM LAGE-1B), AND VARIANT ARG-138.
 RC TISSUE=Placenta;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Klausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 Krausner R.D., Collins F.S., Wagner K.H., Shenmen C.M., Schuler G.D.,
 Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 Hopkins R.F., Jordan H., Moore T., Max S.-I., Wang J., Hsieh F.,
 Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 Scapleton M., Soares M.B., Bonaldi M.F., Casavant T.L., Scheetz T.E.,
 Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
 Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,

RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=LAGE-1B; Synonyms=LAGE-1L;
 CC IsoId=O75638-1; Sequence=Displayed;
 CC Name=LAGE-1A; Synonyms=LAGE-1S;
 CC IsoId=O75638-2; Sequence=VSP_004301;
 CC -!- TISSUE SPECIFICITY: Testis and very low level in placenta and in
 CC some uterus samples. Observed in 25-50% of tumor samples of
 CC melanomas, non-small-cell lung carcinomas, bladder, prostate and
 CC head and neck cancers.
 CC -!- DOMAIN: A transmembrane domain is present in isoform LAGE-1A.
 CC -!- SIMILARITY: Belongs to the CTAG family.
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 CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
 CC or send an email to license@isb-sib.ch).
 CC
 DR EMBL; AJ223093; CAA11117.1; --
 DR EMBL; AJ223093; CAA11116.1; --
 DR EMBL; AJ223040; CAA11043.1; --
 DR EMBL; AJ223041; CAA11044.1; --
 DR EMBL; AJ012834; CAA10194.1; --
 DR EMBL; AJ012835; CAA10196.1; --
 DR EMBL; BC002833; AA02833.1; --
 DR Genew; HGNC:2492; CTAG2.
 DR H-InvDB; HIX0017163; --
 DR MIM; 300396; --
 KW Alternative splicing; Antigen; Polymorphism; Transmembrane.
 FT DOMAIN 5 79 Gly-rich.
 FT DOMAIN 183 198 Poly-Pro.
 FT VARSPLIC 135 210 MSVDDRGAGRMVVGVLGASPEGQKARDLTPKHV
 FT FT SEORPTGPPPPGAGQGGCGRVAFNVMSAPHI -> IR
 FT FT LTAADHRQLQSLSSCLQLSLLMWITQCFPLVFLAQPSSG
 FT FT QRR (in isoform LAGE-1A).
 FT FT /FTId=VSP_004301.
 FT VARIANT 6 6 R -> Q.
 FT /FTId=VAR_007855.
 FT VARIANT 89 89 E -> Q.
 FT /FTId=VAR_007856.
 FT VARIANT 138 138 W -> R.
 FT /FTId=VAR_007857.
 FT SEQUENCE 210 AA; 21119 MW; 8BE0EE00AE55E8BE CRC64;
 SQ
 Query Match 62.0%; Score 595; DB 1; Length 210;
 Best Local Similarity 82.0%; Pred. No. 3.4e-33;
 Matches 109; Conservative 11; Mismatches 13; Indels 0; Gaps 0;
 QY 1 MQAEGRTGSGTGDADGPGGPGIPDGGNAGGPGAGATGGRPGAGAAASGPGGGA 60
 |||||
 Db 1 MQAEGRTGSGTGDADGPGGPGIPDGGNAGGPGAGATGGRPGAGAAASGPGGGA 60
 |||||
 QY 61 PRGPHGGAASGLNGCCRCGARGPESRLLEFYLPAMPFATPMEALARRSLAQDAPPLPVP 120
 |||||
 Db 61 PRGPHGGAASGLNGCCRCGARGPESRLLEFYLPAMPFATPMEALARRSLAQDAPPLPVP 120
 |||||
 QY 121 VLLKFTVSGNLTIRLTAAHRQLQSLSSCLQLSLLMWITQCFPLVFLAQPSPGRR 180
 |||||
 Db 121 VLLKFTVSGNLTIRLTAAHRQLQSLSSCLQLSLLMWITQCFPLVFLAQPSPGRR 180
 |||||
 RESULT 3
 Q9NY13 PRELIMINARY; PRT; 142 AA.
 ID Q9NY13
 AC Q9NY13;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)

DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DE 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
GN Name=LAGE-2;
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Lethe B.G.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ275978; CAB76945.1; -;
KW Hypothetical protein.
FT NON TER 1 1
SQ SEQUENCE 142 AA; 13895 MW; 27EBE922AC4ACC7B CRC64;
Query Match 60.6%; Score 581; DB 2; Length 142;
Best Local Similarity 94.8%; Pred. No. 2.1e-32;
Matches 109; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
QY 27 PGNVAGPGAGATGGRPGAGARASPGGAPRPHGAGASGLNGCCRCGARGPESR 86
DB 1 PGNVAGPGAGATGGRPGAGARASPGGAPRPHGAGASGLNGCCRCGARGPESR 60
QY 87 LLEFYLLAMPATPMEAEALARRSLAQDAPPLPVPGLLKFTVSGNLTIRLTAA 141
DB 61 LLEFYLLAMPATPMEAEALARRSLAQDAPPLPVPGLLKFTVSGNLTMSVQDD 115
RESULT 4
IBA2 HUMAN STANDARD; PRT; 143 AA.
AC Q14657; Q81278;
DT 01-NOV-1997 (Rel. 35, Created)
DT 25-OCT-2004 (Rel. 45, Last sequence update)
DE ITPA2 protein (ESO-3 protein) (DXS9879E).
GN Name=ITPA2; Synonyms=ESO3;
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Blood, and Pancreas;
RX MEDLINE=2238257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieff F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards D., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fehy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalek U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RL and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE OF 2-143 FROM N.A., AND TISSUE SPECIFICITY.
RC TISSUE=Liver;
RX MEDLINE=96374823; PubMed=8786131; DOI=10.1006/geno.1996.0293;
RA Faranda S., Frattini A., Zucchi I., Patrosso C., Milanesi L.,
RA Montagna C., Vezzoni P.;

RT "Characterization and fine localization of two new genes in Xq28 using
the genomic sequence/EST database screening approach."
Genomics 34:323-327(1996).
RN [3]
RP IDENTIFICATION AND TISSUE SPECIFICITY.
RX PubMed=12384295;
RA Alpen B., Guere A.O., Scanlan M.J., Old L.J., Chen Y.-T.;
RT "A new member of the NY-ESO-1 gene family is ubiquitously expressed in
RT somatic tissues and evolutionarily conserved."
RL Gene 297:141-149(2002).
CC -!- TISSUE SPECIFICITY: Ubiquitous.
CC -!- SIMILARITY: Belongs to the CTAG family.
CC -!- CAUTION: Ref.2 sequence differs from that shown due to a
frameshift in position 54.
CC -----
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CC -----
CC EMBL; BC015744; AAH15744.2; -;
DR EMBL; BC062330; AAH62330.1; -;
DR EMBL; X92896; CAA63489.1; ALT_FRAME.
DR MIM; 300060; -;
SQ SEQUENCE 143 AA; 14804 MW; AD164559371449F8 CRC64;
Query Match 23.1%; Score 222; DB 1; Length 143;
Best Local Similarity 42.1%; Pred. No. 6.2e-08;
Matches 67; Conservative 14; Mismatches 52; Indels 26; Gaps 6;
QY 14 DADGPGGPGI PDGPGGNAGCGEAGATGGRGPRGAGARASGPGGAP---RGPHGGAA 69
DB 3 DADADAG-----GGADGDER---GGHSCRG-GVDTAAAPAGAPPAHAPGPGDDAA 50
QY 70 SGLNGCCRCGARGPESRLLEFYLLAMPATPMEAEALARRSLAQDAPPLPVPGLLKFTVTS 129
DB 51 S-----AAGSRMRPHFTLSVFPPTPLEAEIAHGLAPDAE--PHQRVVGKDLTVS 100
QY 130 GNILYRLTAADHRQLQLSISCLQLSLMMITQCFLP 168
DB 101 GRILVVRKAEBCRLRLISVINFLDQLSLVVRTMORFGP 139
RESULT 5
HYDL STRCO STANDARD; PRT; 627 AA.
AC P42534; Q982L7;
DT 01-NOV-1995 (Rel. 32, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Putative polyketide hydroxylase (EC 1.14.13.-) (WHIE ORF VIII).
GN OrderedLocusNames=SC05321; ORFNames=SC6G9.12c;
OS Streptomyces coelicolor.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1902;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=A3(2) / M145;
RX MEDLINE=21996410; PubMed=12000953; DOI=10.1038/417141a;
RA Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
RA Thompson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
RA Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
RA Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
RA Huang C.-H., Kieser T., Larke L., Murphy L.D., Oliver K., O'Neill S.,
RA Rabinowitz B., Rajandream M.A., Rutherford K.M., Rutter S.,
RA Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
RA Warren T., Wietzorrek A., Woodward J.R., Barrell B.G., Parkhill J.,
RA Hopwood D.A.;

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RT coelcolor A3(2).";
RL Nature 417:141-147 (2002) .
RN [2]
RR SEQUENCE OF 1-255 FROM N.A.
RC STRAIN=A3(2);
RX MEDLINE=94075247; PubMed=8253693;
RA Bianco G., Pereda A., Brian P., Mendez C., Chater K.P., Salas J.A.;
RT "A hydroxylase-like gene product contributes to synthesis of a
RL polyketide spore pigment in Streptomyces halstedii.";
RJ J. Bacteriol. 175:8043-8048 (1993).
CC -!- FUNCTION: Involved in developmentally regulated synthesis of a
CC compound biosynthetically related to polyketide antibiotics which
CC is essential for spore color in Streptococcus coelicolor.
CC -!- COFACTOR: FAD (By similarity).
CC -!- SIMILARITY: Belongs to the phea/tfcb FAD monooxygenase family.
-----
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-----
CC EMBL; AL939123; CAB45603.1; -.
DR EMBL; X74213; CAA52289.1; -.
DR PIR; T35608; T35608.
DR InterPro; IPR008160; Collagen.
DR InterPro; IPR007733; Flav_monooxygense.
DR InterPro; IPR002938; Mox_FAD binding.
DR InterPro; IPR003042; Rng_mnoxygenase.
DR Pfam; PF01494; FAD binding 3; 1.
DR Pfam; PF01360; Monooxygenase; 1.
DR PRINTS; PR00420; RNGMNOXGNASE.
DR Complete proteome; FAD; Flavoпротеin; Oxidoreductase.
KW NP_BIND 22 51
FT NE_BIND 309 319 FAD (Potential).
FT FT CONFLICT 60 60 R > A (in Ref. 2).
FT FT CONFLICT 145 145 L -> LH (in Ref. 2).
FT FT CONFLICT 234 234 C > S (in Ref. 2).
FT SEQUENCE 627 AA; 64557 MW; 746E84A2A9E9511C CRC64;
SQ
Query Match 18.2%; Score 174.5; DB 1; Length 627;
Best Local Similarity 42.7%; Pred. No. 0.00039;
Matches 47; Conservative 4; Mismatches 28; Indels 31; Gaps 6;

QY 5 GRGTGSGTGADPGGGPIIDPGCGNAGGPGEAGATGG-RCPRAGAARAASGPGGGAPRG 63
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 409 GRGTGG-PGGPGGGGGLGGPPGGG-TGGPGGPGGPDGPRGAGAPGGGG--G 462

QY 64 PHGGNASGLNGCCFCARGESRLLEFLVLPF-----ATPMEEAE 103
| | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : |
Db 463 PGGG-----GPQRGLNALGYRYPRGVAGDPA TPVPVE 498

RESULT 6
Q6J6NO PRELIMITARY; PRT; 563 AA.
ID Q6J6NO
OS Araneus ventricosus.
OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Araneae;
OX Acneomorphae; Entelegynae; Araneioidea; Araneiidae; Araneus.
OC NCBI_TaxID=182803;
GN Name=Pfi;
LN 563
RE Ren H.-L., Liu Z.-S., Pan F.-G., Wang X.-H., Ren L.-S., Bu X.-J.;
RL Submitted (MAR-2004) to the EMBL/GenBank/DBSJ databases.
DR EMBL: AY587193; AAT36347.1; -
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ID Q7U022 PRELIMINARY; PRT; 1408 AA.
AC Q7U022;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE PE-PGRS FAMILY PROTEIN.
GN Name=PE_PGRS27; OrderedLocusNames=Mb1485c;
OS Mycobacterium bovis.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1765;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=AF2122/97;
RX MEDLINE=22709107; PubMed=12788972; DOI=10.1073/pnas.1130426100;
RA Garnier T., Eiglmeier K., Camus J.-C., Medina N., Mansoor H.,
RA Pryor M., Duthoy S., Grondin S., Lacroix C., Monsempe C., Simon S.,
RA Harris B., Atkin R., Doggett J., Mayes R., Keating L., Wheeler P.R.,
RA Parkhill J., Barrell B.G., Cole S.T., Gordon S.V., Hewinson R.G.;
RT "The complete genome sequence of Mycobacterium bovis.";
RL Proc. Natl. Acad. Sci. U.S.A. 100:7877-7882(2003).
DR EMBL; BX248339; CAD96152.1; -.
DR InterPro; IPR000084; PE region_N.
DR InterPro; IPR002173; PFKB.
DR Pfam; PF00934; PE; 1.
DR ProDom; PD001223; PE_region_N; 1.
DR PROSITE; PS00583; PFKB_KINASES_1; UNKNOWN_2.
KW Complete proteome.
SQ SEQUENCE 1408 AA; 113412 MW; FF4C3685082F11CA CRC64;
* Query Match 16.7%; Score 160.5; DB 2; Length 1408;
* Best Local Similarity 44.7%; Pred. No. 0.007;
* Matches 42; Conservative 3; Mismatches 32; Indels 17; Gaps 4;
QY 5 GRCGTGGSTGDA-----DGGCGGIGIDGPGGNAGGPGGAGATGCGRPGGAGAAASGP 56
Db 207 GGATGGAGGNAGLFGVGGTGGGPGGPGGPGG-PGGPGGVGGTGGAGGLGGLTYGAGGH 265
QY 57 GGGAPRGP-----HG--GAASGLNGCCRCGARG 82
Db 266 GGAGGPGPIGGVGGHGGVGGAGLLGVGGHGGAG 299
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Job time : 240.286 secs

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OM protein - protein search, using sw model

Run on: September 11, 2005, 01:30:14 ; Search time 66 Seconds
(without alignments)
203.588 Million cell updates/sec

Title: US-09-529-206E-4

Perfect score: 959

Sequence: 1 MQAEGRTGCGTGDADPGG.....WITQCFLPVLQAQPPSGRR 180

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*

- 1: /cgn2_6/ptodata/1/iaa/5A-COMB.pep.*
- 2: /cgn2_6/ptodata/1/iaa/5B-COMB.pep.*
- 3: /cgn2_6/ptodata/1/iaa/6A-COMB.pep.*
- 4: /cgn2_6/ptodata/1/iaa/6B-COMB.pep.*
- 5: /cgn2_6/ptodata/1/iaa/PCTUS-COMB.pep.*
- 6: /cgn2_6/ptodata/1/iaa/backfile1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	959	100.0	180	2	US-08-791-495-9
2	959	100.0	180	4	US-09-392-714-25
3	959	100.0	180	4	US-09-165-546B-15
4	959	100.0	180	4	US-09-341-829A-9
5	959	100.0	180	4	US-09-849-602-30
6	953	99.4	180	3	US-08-937-263B-8
7	953	99.4	180	4	US-09-751-798-8
8	814	84.9	180	2	US-08-791-495-7
9	814	84.9	180	4	US-09-341-829A-7
10	589	61.4	210	2	US-08-791-495-5
11	589	61.4	210	4	US-09-341-829A-5
12	160	16.7	745	2	US-09-010-928B-28
13	160	16.7	870	2	US-09-010-928B-2
14	156.5	16.3	633	1	US-08-642-255-73
15	156.5	16.3	1065	1	US-08-642-255-72
16	155.5	16.2	235	2	US-08-529-190B-1
17	155.5	16.2	641	4	US-09-249-585A-3
18	155.5	16.2	641	4	US-09-410-399-4
19	151.5	15.8	1057	3	US-08-931-820-1
20	151.5	15.8	1341	3	US-08-963-825-18
21	151.5	15.8	1341	3	US-09-500-811-18
22	151.5	15.8	1341	3	US-09-570-573-18
23	151.5	15.8	1341	3	US-09-548-608-18
24	151.5	15.8	1461	4	US-09-585-887-9
25	151.5	15.8	1461	4	US-09-289-578-9
26	151.5	15.8	1464	4	US-09-331-347C-21
27	150.5	15.7	907	2	US-09-010-928B-4

28	150	15.6	1008	3	US-09-219-849-8	Sequence 8, Appli
29	150	15.6	1065	1	US-08-642-255-80	Sequence 80, Appl
30	150	15.6	1065	3	US-08-642-246-16	Sequence 16, Appl
31	150	15.6	1065	4	US-09-451-206-16	Sequence 16, Appl
32	150	15.6	1065	5	PCT-US96-06229-16	Sequence 16, Appl
33	149	15.5	166	4	US-09-297-269-41	Sequence 41, Appl
34	148	15.4	857	4	US-09-902-540-12312	Sequence 12312, A
35	146.5	15.3	1806	4	US-09-919-497-56	Sequence 56, Appl
36	145	15.1	492	4	US-08-468-996-11	Sequence 11, Appl
37	145	15.1	1064	1	US-08-642-255-62	Sequence 62, Appl
38	142.5	14.9	1057	3	US-08-931-820-4	Sequence 4, Appli
39	142.5	14.9	1078	3	US-08-963-825-21	Sequence 21, Appl
40	142.5	14.9	1078	3	US-09-500-811-21	Sequence 21, Appl
41	142.5	14.9	1078	3	US-09-570-573-21	Sequence 21, Appl
42	142.5	14.9	1078	3	US-09-548-608-21	Sequence 21, Appl
43	141.5	14.8	1024	3	US-08-931-820-2	Sequence 2, Appli
44	141.5	14.8	1366	3	US-08-963-825-19	Sequence 19, Appl
45	141.5	14.8	1366	3	US-09-500-811-19	Sequence 19, Appl

ALIGNMENTS

RESULT 1
US-08-791-495-9
; Sequence 9, Application US/08791495
; Patent No. 5811519
; GENERAL INFORMATION:
; APPLICANT: Leth, Bernard
; APPLICANT: Lucas, Sophie
; APPLICANT: De Smet, Charles
; APPLICANT: Godelaine, Daniele
; APPLICANT: Boon-Falleur, Thierry
; TITLE OF INVENTION: LL-1 TUMOR SPECIFIC GENES
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wolf, Greenfield & Sacks, P. C.
; STREET: 600 Atlantic Avenue
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/791,495
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Van Amsterdam, John R.
; REGISTRATION NUMBER: 40,212
; REFERENCE/DOCKET NUMBER: L0461/7005
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-720-3500
; TELEFAX: 617-720-2441
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 180 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-791-495-9

Query Match 100.0%; Score 959; DB 2; Length 180;
Best Local Similarity 100.0%; Pred. No. 1.6e-78;
Matches 180; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MQAEGRTGCGTGDADPGGCGIPDGPNGAGATGCGPRGAGAAASGPGGA 60
DB 1 MQAEGRTGCGTGDADPGGCGIPDGPNGAGATGCGPRGAGAAASGPGGA 60


```
;
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, No. 652517man D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: LUD 5466.3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 318-3168
; TELEFAX: (212) 752-5958
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 180
; TYPE: amino acid
; TOPOLOGY: linear
;
US-09-751-798-8

Query Match 99.4%; Score 953; DB 4; Length 180;
Best Local Similarity 99.4%; Pred. No. 5.6e-78;
Matches 179; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MQAEGRTGCGTGDADGPGGPGIPDGGNAGGPGGAGATGGRGPRGAGAARASGPGGGA 60
DB 1 MQAEGRTGCGTGDADGPGGPGIPDGGNAGGPGGAGATGGRGPRGAGAARASGPGGGA 60
QY 61 PRGPHGGAASGLNGCCRCGARGPESRLLEFYLAMPFATPMEAEIARRSLAQDAPPLPVG 120
DB 61 PRGPHGGAASGLNGCCRCGARGPESRLLEFYLAMPFATPMEAEIARRSLAQDAPPLPVG 120
QY 121 VLLKEFTVSGNLTIRLTAAADHRQLQLSSICLQQLSLLMWITQCFLPVFLAQPSPGQRR 180
DB 121 VLLKEFTVSGNLTIRLTAAADHRQLQLSSICLQQLSLLMWITQCFLPVFLAQPSPGQRR 180

RESULT 8
US-08-791-495-7
; Sequence 7, Application US/08791495
; Patent No. 5811519
; GENERAL INFORMATION:
; APPLICANT: Leth, Bernard
; APPLICANT: Lucas, Sophie
; APPLICANT: De Smet, Charles
; APPLICANT: Godelaine, Daniele
; APPLICANT: Boon-Falleur, Thierry
; TITLE OF INVENTION: LL-1 TUMOR SPECIFIC GENES
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Wolf, Greenfield & Sacks, P.C.
; STREET: 600 Atlantic Avenue
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/791,495
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Van Amsterdam, John R.
; REGISTRATION NUMBER: 40,212
; REFERENCE/DOCKET NUMBER: L0461/7005
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-720-3500
; TELEFAX: 617-720-2441
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 180 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
;
US-08-791-495-7

;
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, No. 652517man D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: LUD 5466.3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 318-3168
; TELEFAX: (212) 752-5958
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 180
; TYPE: amino acid
; TOPOLOGY: linear
;
US-09-751-798-8

Query Match 84.9%; Score 814; DB 2; Length 180;
Best Local Similarity 84.4%; Pred. No. 1.6e-65;
Matches 152; Conservative 13; Mismatches 15; Indels 0; Gaps 0;

QY 1 MQAEGRTGCGTGDADGPGGPGIPDGGNAGGPGGAGATGGRGPRGAGAARASGPGGGA 60
DB 1 MQAEGRTGCGTGDADGPGGPGIPDGGNAGGPGGAGATGGRGPRGAGAARASGPGGGA 60
QY 61 PRGPHGGAASGLNGCCRCGARGPESRLLEFYLAMPFATPMEAEIARRSLAQDAPPLPVG 120
DB 61 PRGPHGGAASGLNGCCRCGARGPESRLLEFYLAMPFATPMEAEIARRSLAQDAPPLPVG 120
QY 121 VLLKEFTVSGNLTIRLTAAADHRQLQLSSICLQQLSLLMWITQCFLPVFLAQPSPGQRR 180
DB 121 VLLKEFTVSGNLTIRLTAAADHRQLQLSSICLQQLSLLMWITQCFLPVFLAQPSPGQRR 180

RESULT 9
US-09-341-829A-7
; Sequence 7, Application US/09341829A
; Patent No. 6794131
; GENERAL INFORMATION:
; APPLICANT: Leth, Bernard
; APPLICANT: Lucas, Sophie
; APPLICANT: De Smet, Charles
; APPLICANT: Godelaine, Daniele
; APPLICANT: Boon-Falleur, Thierry
; TITLE OF INVENTION: LAGE-1 TUMOR ASSOCIATED NUCLEIC ACIDS
; FILE REFERENCE: L0461/7066
; CURRENT APPLICATION NUMBER: US/09/341,829A
; CURRENT FILING DATE: 1999-10-18
; PRIOR APPLICATION NUMBER: US 08/791,495
; PRIOR APPLICATION NUMBER: PCT/US98/01445
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Homo sapiens
;
US-09-341-829A-7

Query Match 84.9%; Score 814; DB 4; Length 180;
Best Local Similarity 84.4%; Pred. No. 1.6e-65;
Matches 152; Conservative 13; Mismatches 15; Indels 0; Gaps 0;

QY 1 MQAEGRTGCGTGDADGPGGPGIPDGGNAGGPGGAGATGGRGPRGAGAARASGPGGGA 60
DB 1 MQAEGRTGCGTGDADGPGGPGIPDGGNAGGPGGAGATGGRGPRGAGAARASGPGGGA 60
QY 61 PRGPHGGAASGLNGCCRCGARGPESRLLEFYLAMPFATPMEAEIARRSLAQDAPPLPVG 120
DB 61 PRGPHGGAASGLNGCCRCGARGPESRLLEFYLAMPFATPMEAEIARRSLAQDAPPLPVG 120
QY 121 VLLKEFTVSGNLTIRLTAAADHRQLQLSSICLQQLSLLMWITQCFLPVFLAQPSPGQRR 180
DB 121 VLLKEFTVSGNLTIRLTAAADHRQLQLSSICLQQLSLLMWITQCFLPVFLAQPSPGQRR 180

RESULT 10
US-08-791-495-5
; Sequence 5, Application US/08791495
; Patent No. 5811519
; GENERAL INFORMATION:
; APPLICANT: Leth, Bernard
; APPLICANT: Lucas, Sophie
; APPLICANT: De Smet, Charles
; APPLICANT: Godelaine, Daniele
; APPLICANT: Boon-Falleur, Thierry
; TITLE OF INVENTION: LL-1 TUMOR SPECIFIC GENES
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wolf, Greenfield & Sacks, P.C.
```

```
; STREET: 600 Atlantic Avenue
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/791,495
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Van Amsterdam, John R.
; REGISTRATION NUMBER: 40,212
; REFERENCE/DOCKET NUMBER: L0461/7005
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-720-3500
; TELEFAX: 617-720-2441
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 210 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-791-495-5

; Query Match 61.4%; Score 589; DB 2; Length 210;
; Best Local Similarity 76.6%; Pred. No. 2.6e-45;
; Matches 108; Conservative 15; Mismatches 18; Indels 0; Gaps 0;

QY 1 MQAEGRTGSGTGDADGPGGPGIPDGGNAGGPGGAGATGGRGPRGAGAAASGPGGGA 60
Db 1 MQAEGQGTGSGTGDADGPGGPGIPDGGNAGGPGGAGATGGRGPRGAGAAASGPGGGA 60

QY 61 PRGPHGGAASGLNGCCRCGARGPESRLLEFYLAMFPATPMEALARRSLAQDAPPLVPFG 120
Db 61 PRGPHGGAASGLNGCCRCGARGPESRLLEFYLAMFPATPMEALARRSLAQDAPPLVPFG 120

QY 121 VLLKEFTVSGNLTIRLTAAD 141
Db 121 AVLKDFTVSGNLLFMSVRDQD 141

RESULT 12
US-09-010-928B-28
; Sequence 28, Application US/09010928B
; Patent No. 5994099
; GENERAL INFORMATION:
; APPLICANT: Lewis, Randolph V
; APPLICANT: Hayashi, Cheryl Y
; TITLE OF INVENTION: EXTREMELY ELASTIC SPIDER SILK PROTEIN AND DNA
; TITLE OF INVENTION: CODING THEREFOR
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH
; STREET: 8110 GATEHOUSE RD. SUITE 500E
; CITY: FALLS CHURCH
; STATE: VIRGINIA
; COUNTRY: UNITED STATES OF AMERICA
; ZIP: 22042
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/010,928B
; FILING DATE: 22-JAN-1998
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Murphy Jr., Gerald M
; REGISTRATION NUMBER: 28977
; REFERENCE/DOCKET NUMBER: 1447-109P
; INFORMATION FOR SEQ ID NO: 28:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 745 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-010-928B-28

Query Match 16.7%; Score 160; DB 2; Length 745;
; Best Local Similarity 52.4%; Pred. No. 2.8e-06;
; Matches 43; Conservative 1; Mismatches 32; Indels 6; Gaps 5;

QY 5 GRGTGSGTGDADGPGGPGIPDGGNAGGP-CEAGATGGRGPRGAGAAASGPGG-GAPR 62
Db 508 GFGGFGGPGGFGGPGGAGGPGYGGG-AGGPGGAGGPGYGGAGG--PYGFGGAGGPGY 564

QY 63 GPHG-GAASGLNGCCRCGARGP 83
Db 565 GPGGAGGSGYGLGAGGSGGVGP 586

RESULT 13
US-09-010-928B-2
; Sequence 2, Application US/09010928B
; Patent No. 5994099
; GENERAL INFORMATION:
; APPLICANT: Lewis, Randolph V
; APPLICANT: Hayashi, Cheryl Y
; TITLE OF INVENTION: EXTREMELY ELASTIC SPIDER SILK PROTEIN AND DNA
```

```
; STREET: 600 Atlantic Avenue
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/791,495
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Van Amsterdam, John R.
; REGISTRATION NUMBER: 40,212
; REFERENCE/DOCKET NUMBER: L0461/7005
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-720-3500
; TELEFAX: 617-720-2441
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 210 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-791-495-5

; Query Match 61.4%; Score 589; DB 2; Length 210;
; Best Local Similarity 76.6%; Pred. No. 2.6e-45;
; Matches 108; Conservative 15; Mismatches 18; Indels 0; Gaps 0;

QY 1 MQAEGRTGSGTGDADGPGGPGIPDGGNAGGPGGAGATGGRGPRGAGAAASGPGGGA 60
Db 1 MQAEGQGTGSGTGDADGPGGPGIPDGGNAGGPGGAGATGGRGPRGAGAAASGPGGGA 60

QY 61 PRGPHGGAASGLNGCCRCGARGPESRLLEFYLAMFPATPMEALARRSLAQDAPPLVPFG 120
Db 61 PRGPHGGAASGLNGCCRCGARGPESRLLEFYLAMFPATPMEALARRSLAQDAPPLVPFG 120

QY 121 VLLKEFTVSGNLTIRLTAAD 141
Db 121 AVLKDFTVSGNLLFMSVRDQD 141

RESULT 11
US-09-341-829A-5
; Sequence 5, Application US/09341829A
; Patent No. 6794131
; GENERAL INFORMATION:
; APPLICANT: Leth, Bernard
; APPLICANT: Lucas, Sophie
; APPLICANT: De Smet, Charles
; APPLICANT: Godelaine, Daniele
; APPLICANT: Boon-Faileur, Thierry
; TITLE OF INVENTION: LAGS-1 TUMOR ASSOCIATED NUCLEIC ACIDS
; FILE REFERENCE: L0461/7066
; CURRENT APPLICATION NUMBER: US/09/341,829A
; CURRENT FILING DATE: 1999-10-18
; PRIOR APPLICATION NUMBER: US 08/791,495
; PRIOR APPLICATION NUMBER: PCT/US98/01445
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 210
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-341-829A-5

Query Match 61.4%; Score 589; DB 4; Length 210;
; Best Local Similarity 76.6%; Pred. No. 2.6e-45;
; Matches 108; Conservative 15; Mismatches 18; Indels 0; Gaps 0;
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; TITLE OF INVENTION: CODING THEREFOR
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH
; STREET: 8110 GATEHOUSE RD. SUITE 500E
; CITY: FALLS CHURCH
; STATE: VIRGINIA
; COUNTRY: UNITED STATES OF AMERICA
; ZIP: 22042
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: 22-JAN-1998
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Murphy Jr., Gerald M
; REGISTRATION NUMBER: 28977
; REFERENCE/DOCKET NUMBER: 1447-109P
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 870 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-010-928B-2

Query Match 16.7%; Score 160; DB 2; Length 870;
Best Local Similarity 52.4%; Pred. No. 3.3e-06;
Matches 43; Conservative 1; Mismatches 32; Indels 6; Gaps 5;

Qy 5 GRTGTGSGTADGGGGIPDGGNAGGP-GEAGATGGRGPRGAGAARASGPGG-GAPR 62
Db 634 GPGGFGGPGGFGGPGGAGGPGVFGG-AGGPGGAGGPGVPGGAGG--PYGPGGAGGPV 690

Qy 63 GPHG-GAASGLNGCCRCGARGP 83
Db 691 GPGGAGGSGYGLGGAGSGGSGVGP 712

RESULT 14
US-08-642-255-73
; Sequence 73, Application US/08642255
; Patent No. 5773249
; GENERAL INFORMATION:
; APPLICANT: CAPPELLO, Joseph
; APPLICANT: FERRARI, Franco A.
; TITLE OF INVENTION: High Molecular Weight Collagen-Like
; NUMBER OF SEQUENCES: 135
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FLEHR, HOBRACH, TEST, ALBRITTON & HERBERT
; STREET: 4 Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-4187
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/642,255
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: ROWLAND, Bertram I.
; REGISTRATION NUMBER: 20,015
; REFERENCE/DOCKET NUMBER: A55556-3/BIR
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 494-8700
; TELEFAX: (415) 494-8771
; TELEX: 910 277299 FHT UR
; INFORMATION FOR SEQ ID NO: 72:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1065 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-642-255-72

Query Match 16.3%; Score 156.5; DB 1; Length 1065;
Best Local Similarity 41.7%; Pred. No. 8.6e-06;
Matches 43; Conservative 5; Mismatches 24; Indels 31; Gaps 6;

; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 494-8700
; TELEFAX: (415) 494-8771
; TELEX: 910 277299 FHT UR
; INFORMATION FOR SEQ ID NO: 73:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 633 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-642-255-73

Query Match 16.3%; Score 156.5; DB 1; Length 633;
Best Local Similarity 41.7%; Pred. No. 4.8e-06;
Matches 43; Conservative 5; Mismatches 24; Indels 31; Gaps 6;

Qy 3 AEG-RGTGSGTGD-----ADGPGGPG-----IPDGGNAGGPGSAGATGGRG 44
Db 107 AQPAGPGGSRGDPGPPGAQGPAGPGGSRGDPGPPGAQGPAGPGGSRGDPGPPGAHGPAG 166

Qy 45 PRG-----AGAARASGPGGAPRPHGGAASGLNGCCRCGARGP 83
Db 167 PKGAHGPAGPKGAHGPAG--PKGAHGPAGPK-----GAQGP 200

RESULT 15
US-08-642-255-72
; Sequence 72, Application US/08642255
; Patent No. 5773249
; GENERAL INFORMATION:
; APPLICANT: CAPPELLO, Joseph
; APPLICANT: FERRARI, Franco A.
; TITLE OF INVENTION: High Molecular Weight Collagen-Like
; NUMBER OF SEQUENCES: 135
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FLEHR, HOBRACH, TEST, ALBRITTON & HERBERT
; STREET: 4 Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-4187
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/642,255
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: ROWLAND, Bertram I.
; REGISTRATION NUMBER: 20,015
; REFERENCE/DOCKET NUMBER: A55556-3/BIR
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 494-8700
; TELEFAX: (415) 494-8771
; TELEX: 910 277299 FHT UR
; INFORMATION FOR SEQ ID NO: 72:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1065 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-642-255-72

Query Match 16.3%; Score 156.5; DB 1; Length 1065;
Best Local Similarity 41.7%; Pred. No. 8.6e-06;
Matches 43; Conservative 5; Mismatches 24; Indels 31; Gaps 6;
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OM protein - protein search, using sw model

Run on: September 11, 2005, 01:43:05 ; Search time 243.429 Seconds
(without alignments)
291.657 Million cell updates/sec

Title: US-09-529-206E-4

Perfect score: 959

Sequence: 1 MQAERGTCGGTGADGPGG.....WITQCFPLVFLAQPSPGQRR 180

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1777461 seqs, 394431504 residues

Total number of hits satisfying chosen parameters: 1777461

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

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12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
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17: /cgn2_6/ptodata/1/pubpaa/US10E_PUBCOMB.pep.*
18: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
19: /cgn2_6/ptodata/1/pubpaa/US11A_PUBCOMB.pep.*
20: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
21: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
22: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	959	100.0	180	15	US-10-026-066-3
4	959	100.0	180	15	US-10-117-937-74
5	959	100.0	180	15	US-10-295-027-386
6	959	100.0	180	15	US-10-296-734-832
7	959	100.0	180	15	US-10-188-832-139
8	959	100.0	180	16	US-10-777-053-11
9	959	100.0	180	16	US-10-751-088-15
10	959	100.0	180	16	US-10-657-022-74
11	959	100.0	180	16	US-10-837-217-11
					Sequence 30, Appl
					Sequence 71, Appl
					Sequence 3, Appl
					Sequence 74, Appl
					Sequence 386, App
					Sequence 832, App
					Sequence 139, App
					Sequence 11, Appl
					Sequence 15, Appl
					Sequence 74, Appl
					Sequence 11, Appl

12	959	100.0	180	16	US-10-877-373-9	Sequence 9, Appli
13	959	100.0	180	16	US-10-723-860-1270	Sequence 1270, Ap
14	959	100.0	180	17	US-10-871-708-7	Sequence 7, Appli
15	959	100.0	180	18	US-10-895-523-3	Sequence 3, Appli
16	959	100.0	180	18	US-10-182-506A-3	Sequence 3, Appli
17	959	100.0	180	18	US-10-756-149-5024	Sequence 5024, Ap
18	959	100.0	180	20	US-11-067-064-74	Sequence 74, Appl
19	959	100.0	397	9	US-09-821-883-27	Sequence 27, Appl
20	954	99.5	179	17	US-10-482-029-202	Sequence 202, App
21	953	99.4	180	9	US-09-751-798-8	Sequence 8, Appli
22	953	99.4	180	13	US-10-023-182-8	Sequence 8, Appli
23	918	95.7	180	14	US-10-364-614-14	Sequence 14, Appl
24	821	85.6	180	15	US-10-117-937-75	Sequence 75, Appl
25	821	85.6	180	16	US-10-657-022-75	Sequence 75, Appl
26	821	85.6	180	20	US-11-067-064-75	Sequence 75, Appl
27	814	84.9	180	14	US-10-146-473-69	Sequence 69, Appl
28	814	84.9	180	15	US-10-296-734-834	Sequence 834, App
29	814	84.9	180	16	US-10-468-406-4	Sequence 4, Appli
30	814	84.9	180	16	US-10-877-373-7	Sequence 7, Appli
31	631.5	65.8	135	15	US-10-295-027-388	Sequence 388, App
32	631.5	65.8	135	15	US-10-188-832-141	Sequence 141, App
33	596	62.1	210	14	US-10-157-031-88	Sequence 88, Appl
34	595	62.0	210	15	US-10-117-937-76	Sequence 76, Appl
35	595	62.0	210	16	US-10-657-022-76	Sequence 76, Appl
36	595	62.0	210	20	US-11-067-064-76	Sequence 76, Appl
37	589	61.4	210	16	US-10-877-373-5	Sequence 5, Appli
38	532	55.5	123	16	US-10-777-053-17	Sequence 17, Appl
39	532	55.5	123	16	US-10-837-217-17	Sequence 17, Appl
40	532	55.5	179	16	US-10-777-053-20	Sequence 20, Appl
41	532	55.5	179	16	US-10-837-217-20	Sequence 20, Appl
42	445	46.4	3541	15	US-10-296-734-1454	Sequence 1454, Ap
43	191	19.9	54	15	US-10-447-161-140	Sequence 140, App
44	172	17.9	30	15	US-10-296-734-1400	Sequence 1400, Ap
45	172	17.9	30	15	US-10-296-734-1432	Sequence 1432, Ap

ALIGNMENTS

RESULT 1
US-09-849-602-30
; Sequence 30, Application US/09849602
; Publication No. US20030165834A1
; GENERAL INFORMATION:
; APPLICANT: Scanlan, Matthew J.
; APPLICANT: Old, Lloyd J.
; APPLICANT: Stockert, Elisabeth
; APPLICANT: Chen, Yao-Fseng
; TITLE OF INVENTION: Colon Cancer Antigen Panel
; FILE REFERENCE: L0461/7105(JRV)
; CURRENT APPLICATION NUMBER: US/09/849,602
; CURRENT FILING DATE: 2001-05-04
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 30
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-849-602-30

Query Match	100.0%	Score 959;	DB 10;	Length 180;
Best Local Similarity	100.0%	Pred. No. 1.8e-67;		
Matches 180;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	MQAERGTCGGTGADGPGGCGI	PPGCGNAGGCGEAGATGCGR	PGAGAAASGCGGA 60
DB	1	MQAERGTCGGTGADGPGGCGI	PPGCGNAGGCGEAGATGCGR	PGAGAAASGCGGA 60
QY	61	PRGPHGGAASGLNGCCRGAR	GPESRLLEFYLMWPFATPME	AEALARRSLAQDAPLPVPG 120
DB	61	PRGPHGGAASGLNGCCRGAR	GPESRLLEFYLMWPFATPME	AEALARRSLAQDAPLPVPG 120
QY	121	VLLKEFTVSGNLTIRLTAAD	HRQLQLSISCLQQLSLLMW	ITQCFPLVFLAQPSPGQRR 180

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|||||
Db 121 VLLKEFTVSGNLTIRLTAADHRQLQLSSISCLQLSLLMWITQCFLPVFLAQPSPGQRR 180

RESULT 2
US-10-207-655-71
; Sequence 71, Application US/10207655
; Publication No. US20030118592A1
; GENERAL INFORMATION:
; APPLICANT: Ledbetter, Jeffrey A.
; APPLICANT: Hayden-Ledbetter, Martha S.
; TITLE OF INVENTION: BINDING DOMAIN-IMMUNOGLOBULIN FUSION PROTEINS
; FILE REFERENCE: 390069.401C1
; CURRENT APPLICATION NUMBER: US/10/207,655
; CURRENT FILING DATE: 2002-07-25
; NUMBER OF SEQ ID NOS: 426
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 71
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-207-655-71

Query Match 100.0%; Score 959; DB 14; Length 180;
Best Local Similarity 100.0%; Pred. No. 1.8e-67;
Matches 180; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MQAEGRTGSGTGDADGPGGPGIPDGGNAGGPGGAGATGGRGPRGAGAAASGPGGGA 60
Db 1 MQAEGRTGSGTGDADGPGGPGIPDGGNAGGPGGAGATGGRGPRGAGAAASGPGGGA 60

QY 61 PRGPHGGAASGLNGCCRCGARGPESRLLEFYLLAMPFATPMEAEALARRSLAQDAPPLPVPG 120
Db 61 PRGPHGGAASGLNGCCRCGARGPESRLLEFYLLAMPFATPMEAEALARRSLAQDAPPLPVPG 120

QY 121 VLLKEFTVSGNLTIRLTAADHRQLQLSSISCLQLSLLMWITQCFLPVFLAQPSPGQRR 180
Db 121 VLLKEFTVSGNLTIRLTAADHRQLQLSSISCLQLSLLMWITQCFLPVFLAQPSPGQRR 180

RESULT 3
US-10-026-066-3
; Sequence 3, Application US/10026066
; Publication No. US20030215425A1
; GENERAL INFORMATION:
; APPLICANT: Simard, John J. L.
; APPLICANT: Diamond, David C.
; TITLE OF INVENTION: EPI TOPE SYNCHRONIZATION IN ANTIGEN
; PRESENTING CELLS
; FILE REFERENCE: CTLIMM.21C1C
; CURRENT APPLICATION NUMBER: US/10/026,066
; CURRENT FILING DATE: 2001-12-07
; PRIOR APPLICATION NUMBER: 09/561,074
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 09/560,465
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 09/561,572
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 09/561,571
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: PCT/US01/13806
; PRIOR FILING DATE: 2001-04-27
; NUMBER OF SEQ ID NOS: 89
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-026-066-3

Query Match 100.0%; Score 959; DB 15; Length 180;
Best Local Similarity 100.0%; Pred. No. 1.8e-67;
Matches 180; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 MQAEGRTGSGTGDADGPGGPGIPDGGNAGGPGGAGATGGRGPRGAGAAASGPGGGA 60
Db 1 MQAEGRTGSGTGDADGPGGPGIPDGGNAGGPGGAGATGGRGPRGAGAAASGPGGGA 60

QY 61 PRGPHGGAASGLNGCCRCGARGPESRLLEFYLLAMPFATPMEAEALARRSLAQDAPPLPVPG 120
Db 61 PRGPHGGAASGLNGCCRCGARGPESRLLEFYLLAMPFATPMEAEALARRSLAQDAPPLPVPG 120

QY 121 VLLKEFTVSGNLTIRLTAADHRQLQLSSISCLQLSLLMWITQCFLPVFLAQPSPGQRR 180
Db 121 VLLKEFTVSGNLTIRLTAADHRQLQLSSISCLQLSLLMWITQCFLPVFLAQPSPGQRR 180

RESULT 4
US-10-117-937-74
; Sequence 74, Application US/10117937
; Publication No. US20030220239A1
; GENERAL INFORMATION:
; APPLICANT: CTL IMMUNO THERAPIES CORP.
; APPLICANT: SIMARD, John, J.L.
; APPLICANT: DIAMOND, David, C.
; APPLICANT: LIU, Liping
; APPLICANT: XIE, Zhidong
; TITLE OF INVENTION: EPI TOPE SEQUENCES
; FILE REFERENCE: CTLIMM.027A
; CURRENT APPLICATION NUMBER: US/10/117,937
; CURRENT FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: US 60/282,211
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 60/337,017
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: US 60/363,210
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 602
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 74
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-117-937-74

Query Match 100.0%; Score 959; DB 15; Length 180;
Best Local Similarity 100.0%; Pred. No. 1.8e-67;
Matches 180; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MQAEGRTGSGTGDADGPGGPGIPDGGNAGGPGGAGATGGRGPRGAGAAASGPGGGA 60
Db 1 MQAEGRTGSGTGDADGPGGPGIPDGGNAGGPGGAGATGGRGPRGAGAAASGPGGGA 60

QY 61 PRGPHGGAASGLNGCCRCGARGPESRLLEFYLLAMPFATPMEAEALARRSLAQDAPPLPVPG 120
Db 61 PRGPHGGAASGLNGCCRCGARGPESRLLEFYLLAMPFATPMEAEALARRSLAQDAPPLPVPG 120

QY 121 VLLKEFTVSGNLTIRLTAADHRQLQLSSISCLQLSLLMWITQCFLPVFLAQPSPGQRR 180
Db 121 VLLKEFTVSGNLTIRLTAADHRQLQLSSISCLQLSLLMWITQCFLPVFLAQPSPGQRR 180

RESULT 5
US-10-295-027-386
; Sequence 386, Application US/10295027
; Publication No. US20030232350A1
; GENERAL INFORMATION:
; APPLICANT: Afar, Daniel
; APPLICANT: Aziz, Nataasha
; APPLICANT: Gineberg, Wendy M.
; APPLICANT: Gish, Kurt C.
; APPLICANT: Glynn, Richard
; APPLICANT: Hevezi, Peter A.
; APPLICANT: Mack, David H.
; APPLICANT: Murray, Richard
; APPLICANT: Watson, Susan R.
```

APPLICANT: Eos Biotechnology, Inc.
TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and
FILE REFERENCE: 018501-012500US
CURRENT APPLICATION NUMBER: US/10/295,027
CURRENT FILING DATE: 2002-11-13
PRIOR APPLICATION NUMBER: US 09/663,733
PRIOR FILING DATE: 2000-09-15
PRIOR APPLICATION NUMBER: US 60/350,666
PRIOR FILING DATE: 2001-11-13
PRIOR APPLICATION NUMBER: US 60/335,394
PRIOR FILING DATE: 2001-11-15
PRIOR APPLICATION NUMBER: US 60/332,464
PRIOR FILING DATE: 2001-11-21
PRIOR APPLICATION NUMBER: US 60/334,393
PRIOR FILING DATE: 2001-11-29
PRIOR APPLICATION NUMBER: US 60/340,376
PRIOR FILING DATE: 2001-12-14
PRIOR APPLICATION NUMBER: US 60/347,211
PRIOR FILING DATE: 2002-01-08
PRIOR APPLICATION NUMBER: US 60/347,349
PRIOR FILING DATE: 2002-01-10
PRIOR APPLICATION NUMBER: US 60/355,250
PRIOR FILING DATE: 2002-02-08
PRIOR APPLICATION NUMBER: US 60/356,714
PRIOR FILING DATE: 2002-02-13
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 1386
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 386
LENGTH: 180
TYPE: PRT
ORGANISM: Homo sapiens
US-10-295-027-386

Query Match 100.0%; Score 959; DB 15; Length 180;
Best Local Similarity 100.0%; Pred. No. 1.8e-67;
Matches 180; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MQAEGRTGGSTGDADGPGGPGIPDGGNAGGPGGAGATGGRGPRGAGAAASGPGGA 60
DB 1 MQAEGRTGGSTGDADGPGGPGIPDGGNAGGPGGAGATGGRGPRGAGAAASGPGGA 60
QY 61 PRGPHGGAASGLNGCCRCGARGPESRLLEFYLLAMPFATPMEALARRSLAQDAPLPVPG 120
DB 61 PRGPHGGAASGLNGCCRCGARGPESRLLEFYLLAMPFATPMEALARRSLAQDAPLPVPG 120
QY 121 VLLKEFTVSGNLTIRLTAADHRQLQLSISCLQLQLSLLMWITQCFLPVFLAQPSPGQRR 180
DB 121 VLLKEFTVSGNLTIRLTAADHRQLQLSISCLQLQLSLLMWITQCFLPVFLAQPSPGQRR 180

RESULT 6
US-10-296-734-832
Sequence 832, Application US/10296734
Publication No. US20040054137A1
GENERAL INFORMATION:
APPLICANT: Thompson, Scott A
APPLICANT: Ramshaw, Ian A
TITLE OF INVENTION: Synthetic molecules and uses therefor
FILE REFERENCE: Savine
CURRENT APPLICATION NUMBER: US/10/296,734
CURRENT FILING DATE: 2003-08-04
PRIOR APPLICATION NUMBER: AU PQ7761/00
PRIOR FILING DATE: 2000-05-26
NUMBER OF SEQ ID NOS: 1507
SOFTWARE: PatentIn version 3.2
SEQ ID NO 832
LENGTH: 180
TYPE: PRT
ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: NYSOLA consensus polypeptide

US-10-296-734-832
Query Match 100.0%; Score 959; DB 15; Length 180;
Best Local Similarity 100.0%; Pred. No. 1.8e-67;
Matches 180; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MQAEGRTGGSTGDADGPGGPGIPDGGNAGGPGGAGATGGRGPRGAGAAASGPGGA 60
DB 1 MQAEGRTGGSTGDADGPGGPGIPDGGNAGGPGGAGATGGRGPRGAGAAASGPGGA 60
QY 61 PRGPHGGAASGLNGCCRCGARGPESRLLEFYLLAMPFATPMEALARRSLAQDAPLPVPG 120
DB 61 PRGPHGGAASGLNGCCRCGARGPESRLLEFYLLAMPFATPMEALARRSLAQDAPLPVPG 120
QY 121 VLLKEFTVSGNLTIRLTAADHRQLQLSISCLQLQLSLLMWITQCFLPVFLAQPSPGQRR 180
DB 121 VLLKEFTVSGNLTIRLTAADHRQLQLSISCLQLQLSLLMWITQCFLPVFLAQPSPGQRR 180

RESULT 7
US-10-188-832-139
Sequence 139, Application US/10188832
Publication No. US20040076955A1
GENERAL INFORMATION:
APPLICANT: Mack, David H.
APPLICANT: Azi, Natasha
TITLE OF INVENTION: Methods of Diagnosis of Bladder Cancer, Compositions
TITLE OF INVENTION: and Methods of Screening for Modulators of Bladder
TITLE OF INVENTION: Cancer
FILE REFERENCE: 018501-002330US
CURRENT APPLICATION NUMBER: US/10/188,832
CURRENT FILING DATE: 2002-11-22
PRIOR APPLICATION NUMBER: US 60/302,814
PRIOR FILING DATE: 2001-07-03
PRIOR APPLICATION NUMBER: US 60/310,099
PRIOR FILING DATE: 2001-08-03
PRIOR APPLICATION NUMBER: US 60/343,705
PRIOR FILING DATE: 2001-11-08
PRIOR APPLICATION NUMBER: US 60/350,666
PRIOR FILING DATE: 2001-11-13
PRIOR APPLICATION NUMBER: US 60/372,246
PRIOR FILING DATE: 2002-04-12
NUMBER OF SEQ ID NOS: 207
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 139
LENGTH: 180
TYPE: PRT
ORGANISM: Homo sapiens
US-10-188-832-139

Query Match 100.0%; Score 959; DB 15; Length 180;
Best Local Similarity 100.0%; Pred. No. 1.8e-67;
Matches 180; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MQAEGRTGGSTGDADGPGGPGIPDGGNAGGPGGAGATGGRGPRGAGAAASGPGGA 60
DB 1 MQAEGRTGGSTGDADGPGGPGIPDGGNAGGPGGAGATGGRGPRGAGAAASGPGGA 60
QY 61 PRGPHGGAASGLNGCCRCGARGPESRLLEFYLLAMPFATPMEALARRSLAQDAPLPVPG 120
DB 61 PRGPHGGAASGLNGCCRCGARGPESRLLEFYLLAMPFATPMEALARRSLAQDAPLPVPG 120
QY 121 VLLKEFTVSGNLTIRLTAADHRQLQLSISCLQLQLSLLMWITQCFLPVFLAQPSPGQRR 180
DB 121 VLLKEFTVSGNLTIRLTAADHRQLQLSISCLQLQLSLLMWITQCFLPVFLAQPSPGQRR 180
RESULT 8
US-10-777-053-11
Sequence 11, Application US/10777053
Publication No. US20040132088A1
GENERAL INFORMATION:

```
; APPLICANT: Simard, John J. L.;
; APPLICANT: Diamond, David C.
; APPLICANT: Qiu, Zhiyong
; APPLICANT: Lei, Xiang-Dong
; TITLE OF INVENTION: EXPRESSION VECTORS ENCODING EPITOPES OF
; TARGET-ASSOCIATED ANTIGENS AND METHODS FOR THEIR DESIGN
; FILE REFERENCE: MANK.022C1
; CURRENT APPLICATION NUMBER: US/10/777,053
; CURRENT FILING DATE: 2004-02-10
; PRIOR APPLICATION NUMBER: 10/292,413
; PRIOR FILING DATE: 2002-11-07
; PRIOR APPLICATION NUMBER: 60/336,968
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 979
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Homo Sapien
;
US-10-777-053-11

Query Match 100.0%; Score 959; DB 16; Length 180;
Best Local Similarity 100.0%; Pred. No. 1.8e-67;
Matches 180; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MQAEGRTGSGTGDADGPGGPGIPDGPNGAGGPGGAGATGGRGPRGAGAAASGPGGGA 60
Db 1 MQAEGRTGSGTGDADGPGGPGIPDGPNGAGGPGGAGATGGRGPRGAGAAASGPGGGA 60
QY 61 PRGPHGGAASGLNGCCRCGARGPESRLLEFYLLAMPFATPMEALARRSLAQDAPPLVPVG 120
Db 61 PRGPHGGAASGLNGCCRCGARGPESRLLEFYLLAMPFATPMEALARRSLAQDAPPLVPVG 120
QY 121 VLLKEFTVSGNLTIRLTAADHRQLQLSISSCLQLSLLMWITQCFLPVFLAOPPSGQRR 180
Db 121 VLLKEFTVSGNLTIRLTAADHRQLQLSISSCLQLSLLMWITQCFLPVFLAOPPSGQRR 180

RESULT 9
US-10-751-088-15
; Sequence 15, Application US/10751088
; Publication No. US20040158044A1
; GENERAL INFORMATION:
; APPLICANT: Knuth, Alexander; Jager, Elke; Chen, Yao, Scanlan, Matt;
; APPLICANT: Gure, Ali, Old, Lloyd, Ritter, Gerd
; TITLE OF INVENTION: ISOLATED PEPTIDES CORRESPONDING TO AMINO ACID
; SEQUENCES OF NY-ESO-1, WHICH BIND TO MHC CLASS I AND MHC CL
; USES THEREOF
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FULBRIGHT & JAWORSKI LLP
; STREET: 666 Fifth Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10158
;
COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: word
;
CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/751,088
; FILING DATE: 02-Jan-2004
; CLASSIFICATION: 530
;
PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/165,546D
; FILING DATE: 02-Oct-1998
; APPLICATION NUMBER: 09/062,422
; FILING DATE: April 17, 1998
; APPLICATION NUMBER: 08/937,263
; FILING DATE: September 15, 1997
; APPLICATION NUMBER: US 08/725,182
```

```
; FILING DATE: October 3, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, Norman D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: LUD 2166.4 CIP (09807811)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 318-3000
; TELEFAX: (212) 318-3400
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 180 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 15
US-10-751-088-15

Query Match 100.0%; Score 959; DB 16; Length 180;
Best Local Similarity 100.0%; Pred. No. 1.8e-67;
Matches 180; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MQAEGRTGSGTGDADGPGGPGIPDGPNGAGGPGGAGATGGRGPRGAGAAASGPGGGA 60
Db 1 MQAEGRTGSGTGDADGPGGPGIPDGPNGAGGPGGAGATGGRGPRGAGAAASGPGGGA 60
QY 61 PRGPHGGAASGLNGCCRCGARGPESRLLEFYLLAMPFATPMEALARRSLAQDAPPLVPVG 120
Db 61 PRGPHGGAASGLNGCCRCGARGPESRLLEFYLLAMPFATPMEALARRSLAQDAPPLVPVG 120
QY 121 VLLKEFTVSGNLTIRLTAADHRQLQLSISSCLQLSLLMWITQCFLPVFLAOPPSGQRR 180
Db 121 VLLKEFTVSGNLTIRLTAADHRQLQLSISSCLQLSLLMWITQCFLPVFLAOPPSGQRR 180

RESULT 10
US-10-657-022-74
; Sequence 74, Application US/10657022
; Publication No. US20040180354A1
; GENERAL INFORMATION:
; APPLICANT: Simard, John J. L.
; APPLICANT: Diamond, David C.
; APPLICANT: Liu, Liping
; APPLICANT: Liu, Zheng
; TITLE OF INVENTION: EPITOPE SEQUENCES
; FILE REFERENCE: MANK.032A
; CURRENT APPLICATION NUMBER: US/10/657,022
; CURRENT FILING DATE: 2003-09-04
; PRIOR APPLICATION NUMBER: 60/409123
; PRIOR FILING DATE: 2002-09-06
; NUMBER OF SEQ ID NOS: 610
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 74
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Homo sapiens
;
US-10-657-022-74

Query Match 100.0%; Score 959; DB 16; Length 180;
Best Local Similarity 100.0%; Pred. No. 1.8e-67;
Matches 180; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MQAEGRTGSGTGDADGPGGPGIPDGPNGAGGPGGAGATGGRGPRGAGAAASGPGGGA 60
Db 1 MQAEGRTGSGTGDADGPGGPGIPDGPNGAGGPGGAGATGGRGPRGAGAAASGPGGGA 60
QY 61 PRGPHGGAASGLNGCCRCGARGPESRLLEFYLLAMPFATPMEALARRSLAQDAPPLVPVG 120
Db 61 PRGPHGGAASGLNGCCRCGARGPESRLLEFYLLAMPFATPMEALARRSLAQDAPPLVPVG 120
QY 121 VLLKEFTVSGNLTIRLTAADHRQLQLSISSCLQLSLLMWITQCFLPVFLAOPPSGQRR 180
Db 121 VLLKEFTVSGNLTIRLTAADHRQLQLSISSCLQLSLLMWITQCFLPVFLAOPPSGQRR 180
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RESULT 11
US-10-837-217-11
; Sequence 11, Application US/10837217
; Publication No. US20040203051A1
; GENERAL INFORMATION:
; APPLICANT: Simard, John J. L.
; APPLICANT: Diamond, David C.
; APPLICANT: Qiu, Zhiyong
; APPLICANT: Lei, Xiang-Dong
; TITLE OF INVENTION: EXPRESSION VECTORS ENCODING EPITOPES OF
; TITLE OF INVENTION: TARGET-ASSOCIATED ANTIGENS AND METHODS FOR THEIR DESIGN
; FILE REFERENCE: MANNK 022C2
; CURRENT APPLICATION NUMBER: US/10/837,217
; CURRENT FILING DATE: 2004-04-30
; PRIOR APPLICATION NUMBER: 10/292,413
; PRIOR FILING DATE: 2002-11-07
; PRIOR APPLICATION NUMBER: 60/336,968
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 979
; SOFTWARE: Fast-Seq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-837-217-11

Query Match      100.0%; Score 959; DB 16; Length 180;
Best Local Similarity 100.0%; Pred. No. 1.8e-67;
Matches 180; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MQAEGRTGSGTGDADGPGGPGIPDGGGNAGGPGGAGATGGRGPRGAGAAASGGPGGGA 60
Db 1 MQAEGRTGSGTGDADGPGGPGIPDGGGNAGGPGGAGATGGRGPRGAGAAASGGPGGGA 60
Qy 61 PRGPHGGAASGLNGCCRCGARGPESRLLEFVLAMPFATPMEAEIARSLAQDAPPLVPVG 120
Db 61 PRGPHGGAASGLNGCCRCGARGPESRLLEFVLAMPFATPMEAEIARSLAQDAPPLVPVG 120
Qy 121 VLLKEFTVSGNLTIRLTAAHDHRLQLSISSCQLQLSLLMWITTCFLPVFLAOPPSQRR 180
Db 121 VLLKEFTVSGNLTIRLTAAHDHRLQLSISSCQLQLSLLMWITTCFLPVFLAOPPSQRR 180

RESULT 12
US-10-877-373-9
; Sequence 9, Application US/10877373
; Publication No. US20040234541A1
; GENERAL INFORMATION:
; APPLICANT: Leth,, Bernard
; APPLICANT: Lucas, Sophie
; APPLICANT: De Smet, Charles
; APPLICANT: Godelaine, Daniele
; APPLICANT: Boon-Falleur, Thierry
; TITLE OF INVENTION: LAGE-1 TUMOR ASSOCIATED NUCLEIC ACIDS
; FILE REFERENCE: 10461/7066
; CURRENT APPLICATION NUMBER: US/10/877,373
; CURRENT FILING DATE: 2004-06-25
; PRIOR APPLICATION NUMBER: US/09/341,829
; PRIOR FILING DATE: 1999-10-18
; PRIOR APPLICATION NUMBER: US 08/791,495
; PRIOR APPLICATION NUMBER: PCT/US98/01445
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: Fast-Seq for Windows Version 3.0
; SEQ ID NO 9
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-877-373-9

Query Match      100.0%; Score 959; DB 16; Length 180;
Best Local Similarity 100.0%; Pred. No. 1.8e-67;
Matches 180; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Job time : 244.429 secs

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Query Match      100.0%; Score 959; DB 17; Length 180;
Best Local Similarity 100.0%; Pred. No. 1.8e-67;
Matches 180; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MQAEGRTGSGTGDADGPGGPGIPDGGNAGGPGGAGATGGRGPRGAGAAARASGPGGGA 60
   |||||
Db 1 MQAEGRTGSGTGDADGPGGPGIPDGGNAGGPGGAGATGGRGPRGAGAAARASGPGGGA 60
   |||||

QY 61 PRGPHGGAASGLNGCCRCGARGPESRLLEFYLLAMPFATPMEAEIARRSLAQDAPPLVPVG 120
   |||||
Db 61 PRGPHGGAASGLNGCCRCGARGPESRLLEFYLLAMPFATPMEAEIARRSLAQDAPPLVPVG 120
   |||||

QY 121 VLLKEFTVSGNLTIRLTAAHRLQLSISSCQLQLSLLMWITQCFLPVFLAOPPSGQRR 180
   |||||
Db 121 VLLKEFTVSGNLTIRLTAAHRLQLSISSCQLQLSLLMWITQCFLPVFLAOPPSGQRR 180
   |||||
```

RESULT 15

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US-10-895-523-3
; Sequence 3, Application US/10895523
; Publication No. US20050130920A1
; GENERAL INFORMATION:
; APPLICANT: Simard, John J. L.
; APPLICANT: Lei, Xiang-Dong
; APPLICANT: Diamond, David C.
; TITLE OF INVENTION: EPITOPE SYNCHRONIZATION IN ANTIGEN
; FILE REFERENCE: MANNK.021C1PCC1
; CURRENT APPLICATION NUMBER: US/10/895,523
; CURRENT FILING DATE: 2004-07-20
; PRIOR APPLICATION NUMBER: 10/026,066
; PRIOR FILING DATE: 2001-12-07
; PRIOR APPLICATION NUMBER: 10/005,905
; PRIOR FILING DATE: 2001-12-07
; PRIOR APPLICATION NUMBER: 09/561,074
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 09/560,465
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 09/561,572
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 09/561,571
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: PCT/US01/13806
; PRIOR FILING DATE: 2001-04-27
; PRIOR APPLICATION NUMBER: 09/999,186
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 94
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-895-523-3
```

```
Query Match      100.0%; Score 959; DB 18; Length 180;
Best Local Similarity 100.0%; Pred. No. 1.8e-67;
Matches 180; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MQAEGRTGSGTGDADGPGGPGIPDGGNAGGPGGAGATGGRGPRGAGAAARASGPGGGA 60
   |||||
Db 1 MQAEGRTGSGTGDADGPGGPGIPDGGNAGGPGGAGATGGRGPRGAGAAARASGPGGGA 60
   |||||

QY 61 PRGPHGGAASGLNGCCRCGARGPESRLLEFYLLAMPFATPMEAEIARRSLAQDAPPLVPVG 120
   |||||
Db 61 PRGPHGGAASGLNGCCRCGARGPESRLLEFYLLAMPFATPMEAEIARRSLAQDAPPLVPVG 120
   |||||

QY 121 VLLKEFTVSGNLTIRLTAAHRLQLSISSCQLQLSLLMWITQCFLPVFLAOPPSGQRR 180
   |||||
Db 121 VLLKEFTVSGNLTIRLTAAHRLQLSISSCQLQLSLLMWITQCFLPVFLAOPPSGQRR 180
   |||||
```

Search completed: September 11, 2005, 02:07:10

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 11, 2005, 01:19:58 ; Search time 28.6667 Seconds
(without alignments)
269.833 Million cell updates/sec

Title: US-09-529-206E-4_COPY_43_62
Perfect score: 107
Sequence: 1 RGRGAGARASFGGGAPR 20

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A Geneseq_16Dec04:.*
1: Geneseqp1980s:.*
2: Geneseqp1990s:.*
3: Geneseqp2000s:.*
4: Geneseqp2001s:.*
5: Geneseqp2002s:.*
6: Geneseqp2003as:.*
7: Geneseqp2003bs:.*
8: Geneseqp2004s:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	107	100.0	20	2	AAY05979 Human can
2	107	100.0	179	8	Adk68648 Epitope 1
3	107	100.0	180	2	Aaw62584 Cancer as
4	107	100.0	180	2	Aaw69665 Human NY-
5	107	100.0	180	2	AAY05965 Human can
6	107	100.0	180	3	AAY52430 Human tum
7	107	100.0	180	3	AAY70862 Human tum
8	107	100.0	180	3	AB03154 Human oes
9	107	100.0	180	4	AB69946 Human oes
10	107	100.0	180	4	AAG67164 Amino aci
11	107	100.0	180	4	AAU01535 Human NY-
12	107	100.0	180	4	AAE07714 Human NY-
13	107	100.0	180	5	AAU84818 Human NYN
14	107	100.0	180	5	AAU11543 Human tum
15	107	100.0	180	6	ABR58672 Human can
16	107	100.0	180	6	ABR48210 Human bla
17	107	100.0	180	6	ABU56508 Lung can
18	107	100.0	180	6	ABU56694 Lung can
19	107	100.0	180	6	ABP74198 Human NY-
20	107	100.0	180	6	ABR3438 Human NY-
21	107	100.0	180	7	ADC09576 NY-ESO-1
22	107	100.0	180	7	ADD35568 Human NY-
23	107	100.0	180	7	ADD25510 Binding d
24	107	100.0	180	7	ADN39068 Cancer/an
25	107	100.0	180	8	ADJ54139 Human NY-

26	107	100.0	180	8	ADM72815	Adm72815 Human NY-
27	107	100.0	180	8	ADM73418	Adm73418 CAG-3 pro
28	107	100.0	180	8	ADM73417	Adm73417 Human NY-
29	107	100.0	180	8	ADQ18451	Adq18451 Human sof
30	107	100.0	180	8	ADQ10446	Adq10446 Autoimmun
31	107	100.0	397	4	AAE13122	AAE13122 NY-ESO-IC
32	102	95.3	30	5	AAU85105	AAU85105 Human NYN
33	102	95.3	3541	5	AAU85130	AAU85130 Human mel
34	101	94.4	180	6	ABU64816	ABU64816 Human NY-
35	101	94.4	180	7	ADU35564	ADU35564 Human NY-
36	99	92.5	135	6	ABR58673	ABR58673 Human can
37	99	92.5	135	6	ABR48211	ABR48211 Human bla
38	99	92.5	135	6	ABU56509	ABU56509 Lung can
39	99	92.5	135	6	ABU56695	ABU56695 Lung can
40	99	92.5	135	7	ADN39070	ADN39070 Cancer/an
41	99	92.5	179	8	ADM73424	ADM73424 Consensus
42	99	92.5	180	2	Aaw69664	Aaw69664 Human LAG
43	99	92.5	180	3	AAU70860	AAU70860 Human LAG
44	99	92.5	180	5	AAU84820	AAU84820 Human LAG
45	99	92.5	180	5	ABB78346	ABB78346 Amino aci

ALIGNMENTS

RESULT 1
AAY05979
ID AAY05979 standard; peptide; 20 AA.

AC AAY05979;

XX 16-AUG-1999 (first entry)

XX Human cancer antigen NY ESO-1/CAG-3 ORF1 cancer peptide.

XX NY ESO-1/CAG-3 gene; CAG-3 gene; cancer peptide; antigen; human;
KW leukaemia; non-Hodgkins lymphoma; Hodgkins lymphoma; lung cancer;
KW metastasis; melanoma; adenocarcinoma; thymoma; colon cancer;
KW uterine cancer; breast cancer; prostate cancer; ovarian cancer;
KW cervical cancer; bladder cancer; kidney cancer; pancreatic cancer;
KW liver cancer; sarcoma; tumour; diagnosis; immunotherapy; therapy;
KW vaccine.

XX Homo sapiens.

OS Synthetic.

XX WO9918206-A2.

XX 15-APR-1999.

XX 21-SRP-1998; 98WO-US019609.

XX 08-OCT-1997; 97US-0061428P.

(USSH) US DEPT HEALTH & HUMAN SERVICES.

Wang RF, Rosenberg SA;

WPI; 1999-277270/23.

Cancer antigen NY ESO1/CAG-3.

Claim 16; Page 64; 88pp; English.

The present sequence represents a cancer peptide that is based on amino acid residues 44-62 of human ESO-1/CAG-3 (or CAG-3) ORF1 (see AA05965), a new and potent tumour antigen capable of eliciting an antigen specific immune response by T cells. Cancer peptides derived from CAG-3 ORF1, CAG-3 ORF2 (see AA05966), portions of them and their variants (see AA05967-87), are useful as cancer vaccines that protect against cancer. The invention provides: vectors and host cells (also useful as vaccines); a method of diagnosis of cancer or precancer; a transgenic animal; antisense oligonucleotides that inhibit expression of the cancer peptide

CC or tumour antigen; antibodies reacting with a CAG-3 cancer peptide,
 CC useful in diagnostic and detection assays; and methods for preventing or
 CC inhibiting cancer by administering a cancer peptide, with or without an
 CC HLA molecule. The cancer peptides form part of, or are derived from,
 CC cancers such as primary or metastatic melanoma, thymoma, lymphoma,
 CC sarcoma, lung cancer, liver cancer, leukaemia, uterine cancer, cervical
 CC cancer, bladder cancer, kidney cancer and adenocarcinomas such as breast,
 CC prostate, ovarian, pancreatic and thyroid cancers. Melanoma is treated by
 CC inducing cancer-specific T cells in vitro for subsequent return to a
 CC patient

XX Sequence 20 AA;

Query Match 100.0%; Score 107; DB 2; Length 20;
 Best Local Similarity 100.0%; Pred. No. 9.6e-06;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGPRGAGARASGPGGAPR 20
 |||||
 Db 1 RGPRGAGARASGPGGAPR 20

RESULT 2
 ADK68648
 ID ADK68648 standard; protein; 179 AA.
 AC ADK68648;

XX
 DT 06-MAY-2004 (first entry)

XX Epitope liberation-related NY-ESO-1 protein SeqID11.

XX epitope liberation; substrate; proteasome; cytostatic; antibacterial;
 KW protozoacide; fungicide; T-cell activator; vaccine; housekeeping epitope;
 KW cytotoxic T lymphocyte; CTL; adoptive immunotherapy; neoplastic cell;
 KW virus; bacterium; protozoan; fungus; housekeeping proteasome system;
 KW human.

XX Homo sapiens.

XX US2003228634-A1.

XX 11-DEC-2003.

PF 07-NOV-2002; 2002US-00292413.

XX 07-NOV-2001; 2001US-0336968P.

XX (SIMA/) SIMARD J J L.

PA (DIAM/) DIAMOND D C.

PA (QIUZ/) QIU Z.

PA (LEIX/) LEI X.

XX Simard JUL, Diamond DC, Qiu Z, Lei X;

XX WPI; 2004-167209/16.

DR N-PSDB; ADK68674.

XX Identifying polypeptide suitable for epitope e.g., housekeeping epitope,
 PT liberation by contacting substrate polypeptide comprising epitope of
 PT interest, with proteasome, and assaying for liberation of epitope.

XX Example 2; SEQ ID NO 11; 67pp; English.

XX This invention relates to a novel method of identifying a polypeptide
 CC suitable for epitope liberation, including the steps of identifying an
 CC epitope of interest; providing substrate polypeptide sequence including
 CC the epitope, wherein the substrate permits processing by a proteasome;
 CC contacting the substrate with a composition including the proteasome,
 CC under conditions that support processing of the substrate by proteasome;
 CC and assaying for liberation of epitope. The invention may be useful for
 CC the development of compounds with a cytostatic, antibacterial,
 CC protozoacide or fungicide activity acting as T-cell activators. In

CC addition, the invention may allow development of a vaccine. The invention
 CC is useful for identifying a polypeptide suitable for epitope liberation,
 CC where the epitope is a housekeeping epitope. The compositions comprising
 CC the identified housekeeping epitopes are useful in vitro in vaccine
 CC development or in the generation or expansion of cytotoxic T lymphocyte
 CC (CTL) to be used in adoptive immunotherapy. The invention is also useful
 CC for activating T-cells against neoplastic cells, and cells infected with
 CC virus, bacterium, protozoan or fungus. CTL epitopes are identified based
 CC on the knowledge that such epitopes are, in fact, produced by the
 CC housekeeping proteasome system. Once identified, these epitopes, embodied
 CC as peptides, can be used to successfully immunise or induce therapeutic
 CC CTL responses against housekeeping proteasome expressing target cells in
 CC the host. The present sequence is that of a protein which is related to
 CC the method of the invention.

XX Sequence 179 AA;

Query Match 100.0%; Score 107; DB 8; Length 179;
 Best Local Similarity 100.0%; Pred. No. 7.3e-05;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGPRGAGARASGPGGAPR 20
 |||||
 Db 42 RGPRGAGARASGPGGAPR 61

RESULT 3

AAW62584

ID AAW62584 standard; protein; 180 AA.

XX AAW62584;

XX 17-SEP-1998 (first entry)

DT Cancer associated antigen NY-ESO-1.

DE Cancer associated antigen NY-ESO-1.

XX Cancer associated antigen; NY-ESO-1; regression; progression; onset;

XX cancer; treatment; diagnosis.

XX Homo sapiens.

XX Key Location/Qualifiers

FT Misc-difference 7 /note= "potential myristoylation site"

FT Misc-difference 9 /note= "potential myristoylation site"

FT Misc-difference 11 /note= "potential phosphorylation site"

FT Misc-difference 98 /note= "potential phosphorylation site"

FT Misc-difference 134 /note= "potential phosphorylation site"

FT Misc-difference 138 /note= "potential phosphorylation site"

XX WO9814464-A1.

XX 09-APR-1998.

XX 15-SEP-1997; 97WO-US016335.

XX 03-OCT-1996; 96US-00725182.

XX (LUDW-) LUDWIG INST CANCER RES.

XX Chen Y, Scanlan M, Gure A, Old LJ, Jager E, Knuth A;

XX Drijfhout JW;

XX WPI; 1998-286417/25.

XX N-PSDB; AAV38566.

XX New isolated cancer associated antigen - is used to develop products for
 PT the diagnosis and treatment of cancers and for monitoring cancer therapy.

XX Claim 8; Fig 3; 49pp; English.

XX The present sequence represents a cancer associated antigen. The clone

CC from which the DNA sequence is obtained is designated NY-ESO-1. The

CC specification described a method for determining regression, progression

CC of onset of a cancerous condition, comprising monitoring a sample from a

CC patient with the cancerous condition for a parameter selected from NY-ESO

CC -1 protein, a peptide derived from NY-ESO-1 protein and cytolytic T cells

CC specific for the peptide and an MHC molecule with which it non-covalently

CC complexes. Methods for the treatment of a cancerous condition are also

CC described. The NY-ESO-1 protein and peptides derived from it can be used

CC for diagnosis and treatment of cancers and to monitor the efficacy of a

CC therapeutic regime

XX SQ Sequence 180 AA;

Query Match 100.0%; Score 107; DB 2; Length 180;

Best Local Similarity 100.0%; Pred. No. 7.3e-05;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGRPGAGAAASGPGGGAPR 20

Db 43 RGRPGAGAAASGPGGGAPR 62

RESULT 4

AAW69665

ID AAW69665 standard; protein; 180 AA.

AC AAW69665;

XX 27-OCT-1998 (first entry)

XX Human NY-ESO-1 protein sequence, formerly known as LL-1.2 clone.

XX Human; LAGE-1; tumour associated protein; LL-1; diagnosis; tumour.

XX Homo sapiens.

XX WO9832855-A1.

XX 30-JUL-1998.

XX 27-JAN-1998; 98WO-US001445.

XX 27-JAN-1997; 97US-00791495.

XX (LUDW-) LUDWIG INST CANCER RES.

XX Lethe B, Lucas S, De Smet C, Godelaine D, Boon-Palleur T;

XX WPI: 1998-427951/36.

XX N-PSDB; AAV50348.

XX New isolated LAGE-1 tumour associated nucleic acids - used to develop

XX products for the diagnosis and treatment of LAGE-1 associated disorders,

XX particularly tumours.

XX Example 2; Page 57-58; 73pp; English.

XX The present sequence represents human NY-ESO-1, formerly known as LL-1.2

CC clone, which is used in an example from the present invention which

CC describes LAGE-1 tumour associated protein (TAP). The present invention

CC also describes: (1) a method for treating a subject with a disorder

CC characterised by expression of a LAGE-1 nucleic acid molecule or an

CC expression product, comprising administering to the subject autologous

CC cytolytic T cells to ameliorate the disorder, where the cytolytic T cells

CC are specific for complexes of an HLA molecule and a LAGE-1 TAP or an

CC immunogenic fragment; (2) a method for treating a subject with a disorder

CC characterised by expression of a LAGE-1 nucleic acid molecule or an

CC expression product, comprising administering a LAGE-1 TAP or an

CC immunogenic fragment to ameliorate the disorder; and (3) a method for

CC selectively enriching a population of T cells with cytolytic T cells

CC specific for a LAGE-1 TAP comprising contacting an isolated population of

CC T cells with an agent presenting a complex of a LAGE TAP or an

CC immunogenic fragment and a HLA presenting molecule to selectively enrich

CC the isolated population of T cells with the cytolytic T cells. The

CC methods and products from the present invention can be used for the

CC diagnosis and treatment of LAGE-1 associated disorders, particularly

XX SQ Sequence 180 AA;

Query Match 100.0%; Score 107; DB 2; Length 180;

Best Local Similarity 100.0%; Pred. No. 7.3e-05;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGRPGAGAAASGPGGGAPR 20

Db 43 RGRPGAGAAASGPGGGAPR 62

RESULT 5

AAV05965

ID AAV05965 standard; protein; 180 AA.

XX AAY05965;

XX 16-AUG-1999 (first entry)

XX Human cancer antigen NY ESO-1/CAG-3 ORF1 protein.

XX NY ESO-1/CAG-3 gene; CAG-3 gene; cancer antigen; human; leukaemia;

XX non-Hodgkins lymphoma; Hodgkins lymphoma; lung cancer; metastasis;

XX melanoma; adenocarcinoma; thymoma; colon cancer; uterine cancer;

XX breast cancer; prostate cancer; ovarian cancer; cervical cancer;

XX bladder cancer; kidney cancer; pancreatic cancer; liver cancer; sarcoma;

XX tumour; diagnosis; immunotherapy; therapy; vaccine; ORF1.

XX Homo sapiens.

XX WO9918206-A2.

XX 15-APR-1999.

XX 21-SEP-1998; 98WO-US019609.

XX 08-OCT-1997; 97US-0061428P.

XX (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX Wang RF, Rosenberg SA;

XX WPI: 1999-277270/23.

XX N-PSDB; AAX58599.

XX Cancer antigen NY ESO1/CAG-3.

XX Claim 4; Fig 3A; 88pp; English.

XX The present sequence represents the ORF1 protein encoded by open reading

CC frame 1 of the human ESO-1/CAG-3 (or CAG-3) gene. CAG-3 is a new and

CC potent tumour antigen capable of eliciting an antigen specific immune

CC response by T cells. Cancer peptides comprising ORF1, ORF2 (see

CC AAY05966), portions of these peptides and their variants (see AAY05965-

CC 87), are useful as cancer vaccines that protect the recipient from

CC development of cancer. The invention provides: vectors and host cells

CC (also useful as vaccines); a method of diagnosis of cancer or precancer;

CC a transgenic animal; antisense oligonucleotides that inhibit expression

CC of the cancer peptide or tumour antigen; antibodies reacting with the CAG

CC -3 cancer peptide, useful in diagnostic and detection assays; and methods

CC for preventing or inhibiting cancer by administering a cancer peptide,

CC with or without an HLA molecule. The cancer peptides form part of, or are

CC derived from, cancers such as primary or metastatic melanoma, thymoma,

CC lymphoma, sarcoma, lung cancer, liver cancer, leukaemia, uterine cancer,

CC ovarian cancer, thyroid cancer, bladder cancer, or lymphoma) and to
 CC simulate the proliferation of T cells

CC Revised record issued on 21-OCT-2004 : Correction to feature table key

XX Sequence 180 AA;

Query Match 100.0%; Score 107; DB 3; Length 180;

Best Local Similarity 100.0%; Pred. No. 7.3e-05;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGRGAGAAARASGGGAPR 20

DB 43 RGRGAGAAARASGGGAPR 62

RESULT 7

AAAY70862

ID AAY70862 standard; protein; 180 AA.

XX AAY70862;

XX 31-JUL-2000 (first entry)

DE Human tumour antigen, NY-ESO-1 protein.

XX NY-ESO-1; CAMEL; CTL-Recognised Antigen on MELanoma; human; cancer; CTL;
 KW cytotoxic T lymphocyte; tumour-associated antigen; LAGE-1; anticancer;
 KW melanoma; immunotherapy; immune response.

XX Homo sapiens.

XX WO200023584-A1.

XX 27-APR-2000.

XX 15-OCT-1999; 99WO-EP007832.

XX 16-OCT-1998; 98EP-00119583.

XX (BOEH) BOEHRINGER INGELHEIM INT GMBH.

XX (UYHO-) UNIV HOSPITAL LEIDEN.

XX Schrier PI, Aarnoudse CA, Heider K, Klade C;

XX WPI; 2000-339685/29.

XX N-PSDB; AAD00152.

PT Tumor-associated antigen useful for cancer immunotherapy is encoded by
 PT the open reading frame of LAGE-1 (a tumor-specific antigen) cDNA.

XX Example 3; Page 62-63; 73pp; English.

CC The present sequence is the human NY-ESO-1 protein, a tumour antigen,
 CC identified by screening an esophagus carcinoma cDNA library. This protein
 CC is derived from open reading frame (ORF)-1 that contain epitopes of
 CC tumour specific T-cells. NY-ESO-1 is expressed in different tumour types,
 CC but not in healthy tissues except in testis. It also shows homology with
 CC the CAMEL (Cytotoxic T lymphocytes (CTL)-recognised Antigen on MELanoma)
 CC protein, a tumour-associated antigen. The tumour-associated antigen
 CC displayed on melanoma cells is recognised by cytotoxic T lymphocytes.
 CC This sequence has anticancer activity. CAMEL tumour antigen and
 CC immunogenic peptides derived from it are useful for cancer immunotherapy.
 CC They have the potential to induce an immune response, by eliciting a CTL
 CC response. The DNA molecule is used for the construction of recombinant or
 CC fusion proteins

XX Sequence 180 AA;

Query Match 100.0%; Score 107; DB 3; Length 180;

Best Local Similarity 100.0%; Pred. No. 7.3e-05;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGRGAGAAARASGGGAPR 20

DB 43 RGRGAGAAARASGGGAPR 62

RESULT 8

AAB03154

ID AAB03154 standard; protein; 180 AA.

XX AC AAB03154;

XX 23-OCT-2000 (first entry)

XX Human oesophageal cancer-associated antigen NY-ESO-1.

XX Oesophageal cancer associated antigen; NY-ESO-1; human; immunogen;

XX Oesophageal carcinoma; melanoma; ovary; testis; transmembrane domain;

XX antibody; diagnostic marker; drug delivery target.

XX Homo sapiens.

XX Key

XX Modified-site

XX Modified-site

XX Modified-site

XX Modified-site

XX Modified-site

XX Modified-site

XX Modified-site

XX Modified-site

XX Modified-site

XX Modified-site

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XX Modified-site

CC generate anti-NY-ESO-1 antibodies. It can also be used as a diagnostic
 CC marker for oesophageal cancer, and can be utilised as a marker for the
 CC targeted delivery of therapeutic agents to oesophageal cancer cells. It
 CC can also be used to generate diagnostic or therapeutic agents
 XX
 SQ Sequence 180 AA;

Query Match 100.0%; Score 107; DB 3; Length 180;
 Best Local Similarity 100.0%; Pred. No. 7.3e-05;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGRPGAGAAARASGPGGGAPR 20
 |||||
 Db 43 RGRPGAGAAARASGPGGGAPR 62

RESULT 9
 AAB69946
 ID AAB69946 standard; protein; 180 AA.

AC AAB69946;

XX 27-APR-2001 (first entry)

XX Human NY-ESO-1 protein.

XX Human; NY-ESO-1; HLA; human leukocyte antigen; CTL; cytotoxic T cell;
 KW HLA-A2; HLA-DR53; melanoma; adenocarcinoma; bladder carcinoma;
 KW non-small cell lung carcinoma; tumour status determination.

XX Homo sapiens.

XX WO200107917-A1.

XX 01-FEB-2001.

XX 14-JUL-2000; 2000WO-US019220.

XX 23-JUL-1999; 99US-00359503.

XX (LUDW-) LUDWIG INST CANCER RES.

PA (SLOK) SLOAN KETTERING INST CANCER RES.

PA (CORR) CORNELL RES FOUND INC.

XX Jager E, Stockert E, Old LJ, Knuth A, Chen Y, Scanlan M;

XX WPI; 2001-182822/18.

DR N-PSDB; AAF58634.

XX Method useful for determining the status (e.g. progression, regression or
 PT stability of the disease) of a cancerous condition, involves determining
 PT the levels of NY-ESO-1 specific antibodies in a sample taken from a
 PT patient.

XX Example 5; Fig 3; 50pp; English.

XX The present sequence is human NY-ESO-1 protein. It is provided in a
 CC specification relating to a method for determining the status of a
 CC cancerous condition in a patient with a tumour that expresses NY-ESO-1.
 CC The method comprises assaying a sample taken from the patient for
 CC antibodies that specifically bind to the NY-ESO-1 and comparing the value
 CC obtained to a prior value obtained from assay of a prior sample taken
 CC from the patient. Any difference between the values is indicative of a
 CC change in status of the cancerous condition. The method is useful for
 CC determining whether a cancerous condition is progressing, regressing or
 CC remaining stable, in particular in patients receiving treatment for a
 CC melanoma, adenocarcinoma, non-small cell lung carcinoma or bladder
 CC carcinoma

XX Sequence 180 AA;

Query Match 100.0%; Score 107; DB 4; Length 180;
 Best Local Similarity 100.0%; Pred. No. 7.3e-05;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RGRPGAGAAARASGPGGGAPR 20
 |||||
 Db 43 RGRPGAGAAARASGPGGGAPR 62

RESULT 10
 AAG67164
 ID AAG67164 standard; protein; 180 AA.

XX AAG67164;

XX 13-NOV-2001 (first entry)

XX Amino acid sequence of cancer testis tumour antigen NY-ESO-1.

XX Cancer testis tumour antigen; NY-ESO-1; LAGE-2; human leukocyte antigen;
 KW HLA; HLA binding peptide; major histocompatibility complex; MHC; tumour;
 KW cancer; testis tumour.

XX Homo sapiens.

XX WO200162917-A1.

XX 30-AUG-2001.

XX 22-JAN-2001; 2001WO-US002126.

XX 22-FEB-2000; 2000US-00510635.

XX (LUDW-) LUDWIG INST CANCER RES.

XX Lethe B, Boon-Falleur T;

XX WPI; 2001-550091/61.

DR N-PSDB; AAH75118.

XX Genomic sequences of tumor associated antigen EY-ESO-1 (LAGE-2) useful
 PT for diagnosing testicular tumors.

XX Example 5; Fig 3; 50pp; English.

XX The present sequence represents cancer testis tumour antigen NY-ESO-1
 CC (also called LAGE-2). NY-ESO-1 is a molecule that is processed to at
 CC least one human leukocyte antigen (HLA) binding peptide, which binds to
 CC Class I and Class II major histocompatibility complex (MHC). NY-ESO-1 is
 CC expressed in tumour mRNA and in testis, but not normal colon, kidney,
 CC liver or brain tissue. The presence or level of expression of NY-ESO-1
 CC may be assayed for the diagnosis of cancer, especially testis tumours

XX Sequence 180 AA;

Query Match 100.0%; Score 107; DB 4; Length 180;
 Best Local Similarity 100.0%; Pred. No. 7.3e-05;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGRPGAGAAARASGPGGGAPR 20
 |||||
 Db 43 RGRPGAGAAARASGPGGGAPR 62

RESULT 11
 AAU01535
 ID AAU01535 standard; protein; 180 AA.

XX AAU01535;

XX 18-JUL-2001 (first entry)

XX Human NY-ESO-1 tumour rejection antigen precursor protein.

XX NY-ESO-1; human; tumour rejection antigen precursor; SSX-2; MHC Class II;

KW major histocompatibility complex; helper T cell; HLA-DR; cancer;
KW human leukocyte antigen-determining region; disease progression;
KW disease regression; disease onset; body tissue; body fluid; enzyme label;
KW radioactive label; monoclonal antibody.

OS Homo sapiens.

	Key	Location/Qualifiers
FH		

FT	Modified-site	7

```
FT /note= "Myristoylated"
```

FT	Modified-site	9
cm		

FT	Modified-site	11	/note= "Myristoylated"
----	---------------	----	------------------------

FI
Modelled-site
FI
ET
/note= "phosphorylated"

FT	Modified-site	98

FT /note= "Phosphorylated"

FT	Modified-site	134
----	---------------	-----

1000

FT	Modified-site	138	/not a "phospho"
FT	Modified-site	138	/not a "phospho"

F1
XX
/note= "Phosp

PN WO200123560-A2

XX

PD 05-APR-2001.

XX

PF	XX	26-SEP-2000; 2000WO-US026411.
PR	XX	29-SEP-1999; 99US-00408036.
PA	XX	(LUDW-) LUDWIG INST CANCER RES.
PI	XX	Tureci O, Sahin U, Pfreundschuh M;
PT	XX	WPI; 2001-266156/27.
DR	XX	N-PSDB; AAS02254.
PT	XX	Polypeptides binding to major histocompatibility complex class II human
PT	XX	leukocyte antigen-determining region molecule having amino acid sequence
PT	XX	found in tumor rejection antigen precursor used for stimulating
PT	XX	proliferation of helper T cells.

PS Claim 4: Fig 3: 62pp: English.

The sequence represents a human NY-ESO-1 tumour rejection antigen precursor. NY-ESO-1 and SSX-2 polypeptides, or fragments of, bind to major histocompatibility complex (MHC) Class II molecules such as human leukocyte antigen-determining region (HLA-DR) molecules and stimulate proliferation of helper T cells. The peptides can be administered to an HLA-DR positive subject in order to stimulate the helper T cells. An MHC Class II HLA-DR-NY-ESO-1/SSX-2 complex expressed on the surface of a cell or present in free form is useful for this stimulation. The nucleic acid is useful for screening for a cancerous condition, which involves contacting a subject sample to a cell line transfected with the immunoreactive cell (helper T cell), where interaction is indicative of cancer. In addition, a sample from a patient (for example, a body fluid or tissue) can be monitored for the amount of the complex present in the bloodstream. This is useful for determining regression, progression or onset of a cancerous condition. The method involves contacting the sample with a radioactive labelled or enzyme labelled monoclonal antibody which specifically binds with the complex.

Sequence 180 AA;

Query Match	100.0%	Score 107;	DB 4;	Length 180;
Best Local Similarity	100.0%;	Pred. No. 7.3e-05;		
Matches 20;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

QY 1 RGPRGAGAAASGPGGGAPR 20

RESULT 12

AAE07714	
ID	AAE07714 standard; protein; 180 AA.
XX	
XX	AAE07714;
XX	
DT	06-NOV-2001 (first entry)
XX	
DE	Human NY ESO-1 protein.
XX	
KW	Human; major histocompatibility complex; MHC class II restricted T cell epitope; MHC-II e
KW	tumour-specific humoral-mediated immunity; c
KW	immunotherapy.
XX	
OS	Homo sapiens.
XX	
FH	Key Location/Qualifiers
FT	Misc-difference 45..47
FT	/note= "Encoded by CCCCCGGGC"

PN WO200155393-A2.

XX XX

PD 02-AUG-2001.

XX

PF 26-JAN-2001; 2001WO-US002765.

	C
	A
	C
	C
	T
	Z
	C
	T
	C
	C
	C
	C
	.
	C
	C
	C
	T
	T
	C
	C
X	E

PR 28-JAN-2000; 2000US-0179004P.
PP 28-SEP-2000; 2000US-0227107P.
PP 29-SEP-2000; 2000US-0227107P.

XX
PR
ZF-SFF-Z0005

PA (USSH) US DEPT HEALTH & HU

XX Wang R, Rosenberg SA, Zeng G;
PI
XX WFI; 2001-496851/54.
DR N-PSDE; AAD14179, AAD14180.
DR
XX New NY-ESO cancer peptide or MHC class II restricted T cell epitopes,
PT useful as immunogen and vaccine for inhibiting cancer in a mammal or as
PT protection from metastasis.

Example 1; Fig 1; 134pp; English.

The invention relates to the identification and isolation of major histocompatibility (MHC) class II restricted T cell epitope (MHC-II epitope) derived from the cancer antigen, NY ESO-1. The MHC-II epitopes from NY ESO-1 are recognised by CD4+ T lymphocytes in an human leucocyte antigen (HLA) class II restricted manner, in particular HLA-DR or HLA-DP restricted. The products of the gene are promising candidates for immunotherapeutic strategies for the prevention, treatment and diagnosis of patients with cancer. The cancer epitopes are useful as immunogen and vaccine to inhibit or to prevent cancer in a mammal by eliciting CD4+ T lymphocytes resulting in protection of the recipient from development of cancer and protection from metastasis, or by inhibiting the growth of cancer cells expressing the NY-ESO-1 gene product. The cancer peptides are also useful as diagnostic agent to detect the presence of cancer, to enhance the generation of antibody and/or CD8+ T cell responses against any given target antigen and/or hapten and to induce tumour-specific humoral-mediated immunity against cancer. The present sequence is human NY ESO-1 protein

Sequence 180 AA;

Query Match	100.0%	Score 107;	DB 4;	Length 180;
Best Local Similarity	100.0%;	Pred. No. 7.3e-05;		
Matches 20;	Conservative	0;	Mismatches 0;	Indels 0;
Matches 20;	Conservative	0;	Mismatches 0;	Indels 0;

1 RGPRGAGAAASGPGGGAPR 20

RESULT 13

CC target cell protein from which epitopes of the invention may be derived,
CC NY-ESO (a tumour associated antigen)
XX
SQ Sequence 180 AA;

Query Match 100.0%; Score 107; DB 5; Length 180;
Best Local Similarity 100.0%; Pred. No. 7.3e-05;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGPARGAARASGPGGAPR 20
|||||
Db 43 RGPARGAARASGPGGAPR 62

RESULT 15

ABR58672
ID ABR58672 standard; protein; 180 AA.

XX ABR58672;

XX 09-JUL-2003 (first entry)

XX Human cancer related protein SEQ ID NO:329.

XX Human; cancer; diagnosis; screening; modulator; leukaemia; ischaemia;
KW heart disease; atherosclerosis; endometriosis.

XX Homo sapiens.

XX WO2003025139-A2.

XX 27-MAR-2003.

XX 17-SEP-2002; 2002WO-US029560.

XX 17-SEP-2001; 2001US-0323469P.

XX 20-SEP-2001; 2001US-0323887P.

XX 13-NOV-2001; 2001US-0350666P.

XX 08-FEB-2002; 2002US-0355145P.

XX 08-FEB-2002; 2002US-0355257P.

XX 12-APR-2002; 2002US-0372246P.

XX (EOSB-) EOS BIOTECHNOLOGY INC.

XX Afar D, Aziz N, Gish KC, Hevezi PA, Mack DH, Wilson KE;

XX Zlotnik A;

XX WPI; 2003-354600/33.

XX N-PSDB; ACC72823.

XX New genes that are up-regulated or down-regulated in cancers, useful as

XX markers for diagnosing e.g. cancer, ischemia or heart diseases, or as

XX therapeutic targets for screening drugs for treating these diseases.

XX Claim 12; Page 757-758; 767pp; English.

XX The present invention describes an isolated nucleic acid molecule, which

XX comprises the sequence of any of the genes that are up-regulated or down-

XX regulated in specific cancers (e.g. about 1031 genes up-regulated in

XX acute lymphocytic leukemia). ACC72841 to ACC72860 represent cancer

XX related gene nucleotide sequences which encode the proteins given in

XX ABR58521 to ABR58709. Also described: (1) determining the presence or

XX absence of a pathological cell in a patient; (2) an expression vector

XX comprising a nucleic acid molecule described above; (3) a host cell

XX comprising the vector; (4) an isolated polypeptide, which is encoded by

XX the nucleic acid; (5) an antibody that specifically binds the polypeptide

XX of (4); (6) specifically targeting a compound to a pathological cell in a

XX patient by administering to the patient the antibody above; and (7) a

XX drug screening assay. The nucleic acid is useful as diagnostic markers or

XX therapeutic targets. In particular, the nucleic acid is useful for

XX diagnosing a pathology, e.g. cancer (e.g. cancer of the bone marrow,

XX bladder, brain, breast, cervix, colon/rectum, kidney, lung, ovary,

XX pancreas, prostate, skin and uterus), wounds, ischaemia, heart diseases,

CC atherosclerosis and endometriosis. The nucleic acid is also useful in
CC drug screening, particularly for identifying agents for treating these
CC pathologies
XX
SQ Sequence 180 AA;

Query Match 100.0%; Score 107; DB 6; Length 180;
Best Local Similarity 100.0%; Pred. No. 7.3e-05;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGPARGAARASGPGGAPR 20
|||||
Db 43 RGPARGAARASGPGGAPR 62

Search completed: September 11, 2005, 01:38:04

Job time : 28.6667 secs

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Qy 2 GPRGAGAAASGPGGG--APR 20
 ||||| | | | | |
 Db 5 GPRGAGRRRTQGRGGGDTPT 25

RESULT 3
 S51604
 C;Species: Rattus norvegicus (Norway rat)
 C;Date: 07-May-1995 #sequence_revision 21-Jul-1995 #text_change 29-May-1998
 C;Accession: S51604
 R;Maisonpierrre, P.C.; Barrezueta, N.X.; Yancopoulos, G.D.
 Oncogene 8, 3277-3286, 1993
 A;Title: Etk-1 and Etk-2: two novel members of the Eph receptor-like tyrosine kinase fam
 A;Reference number: S49015; MUID:94067777; PMID:7504232
 A;Accession: S51604
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-981 <MAI>
 A;Cross-references: EMBL:S68029
 A;Note: the authors translated the codon GAC for residue 170 as Glu
 C;Superfamily: protein-tyrosine kinase, receptor type eph; fibronectin type III repeat h
 C;Keywords: ATP; transmembrane protein
 F;651-917/Domain: protein kinase homology <KIN>
 F;659-667/Region: protein kinase ATP-binding motif

Query Match 56.1%; Score 60; DB 2; Length 981;
 Best Local Similarity 61.9%; Pred. No. 19;
 Matches 13; Conservative 0; Mismatches 6; Indels 2; Gaps 1;

Qy 2 GPRGAGAAASGPGGG--APR 20
 ||||| | | | | |
 Db 5 GPRGAGRRRTQGRGGGDTPT 25

RESULT 4
 S49015
 C;Species: Rattus norvegicus (Norway rat)
 C;Date: 14-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 09-Jul-2004
 C;Accession: S49015; S51602
 R;Maisonpierrre, P.C.; Barrezueta, N.X.; Yancopoulos, G.D.
 Oncogene 8, 3277-3286, 1993
 A;Title: Etk-1 and Etk-2: two novel members of the Eph receptor-like tyrosine kinase fam
 A;Reference number: S49015; MUID:94067777; PMID:7504232
 A;Accession: S49015
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-1005 <MAI>
 A;Cross-references: UNIPROT:P54757; EMBL:S68024
 A;Note: the authors translated the codon GAC for residue 170 as Glu
 A;Accession: S51602
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-305, 'G', 359-1005 <MA2>
 A;Cross-references: EMBL:S68026
 A;Note: the authors translated the codon GAC for residue 170 as Glu
 C;Superfamily: protein-tyrosine kinase, receptor type eph; fibronectin type III repeat h
 C;Keywords: ATP; transmembrane protein
 F;675-941/Domain: protein kinase homology <KIN>
 F;683-691/Region: protein kinase ATP-binding motif

Query Match 56.1%; Score 60; DB 2; Length 1005;
 Best Local Similarity 61.9%; Pred. No. 19;
 Matches 13; Conservative 0; Mismatches 6; Indels 2; Gaps 1;

Qy 2 GPRGAGAAASGPGGG--APR 20
 ||||| | | | | |
 Db 5 GPRGAGRRRTQGRGGGDTPT 25

RESULT 5

OTHUSB
 cytochrome-c oxidase (EC 1.9.3.1) chain Vb precursor - human
 C;Species: Homo sapiens (man)
 C;Date: 31-Mar-1992 #sequence_revision 07-Jun-1996 #text_change 09-Jul-2004
 C;Accession: J03024; A39063; S74198; A28817
 R;Zeviani, M.; Sakoda, S.; Sherbany, A.A.; Nakase, H.; Rizzuto, R.; Samitt, C.E.; DiMa
 Gene 65, 1-11, 1988
 A;Title: Sequence of cDNAs encoding subunit Vb of human and bovine cytochrome c oxidase
 A;Reference number: J03024; MUID:88284368; PMID:2840351
 A;Accession: J03024
 A;Molecule type: mRNA
 A;Residues: 1-129 <ZEV>
 A;Cross-references: UNIPROT:P10606; UNIPROT:Q99610; EMBL:M19961; NID:G180940; PIDN:AAAS
 R;Lomax, M.I.; Hsieh, C.L.; Darvas, B.T.; Francke, U.
 Genomics 10, 1-9, 1991
 A;Title: Structure of the human cytochrome c oxidase subunit Vb gene and chromosomal ma
 A;Reference number: A39063; MUID:91257815; PMID:1646156
 A;Accession: A39063
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-108, 'E', 110-129 <LOM>
 A;Cross-references: EMBL:M59250
 A;Note: the authors translated the codon GGC for residue 21 as His
 R;Bachman, N.J.; Yang, T.L.; Dasen, J.S.; Ernst, R.E.; Lomax, M.I.
 Arch. Biochem. Biophys. 333, 152-162, 1996
 A;Title: Phylogenetic footprinting of the human cytochrome c oxidase subunit Vb promote
 A;Reference number: S74198; MUID:96400390; PMID:8806766
 A;Accession: S74198
 A;Status: translation not shown
 A;Molecule type: DNA
 A;Residues: 1-35, 'TR' <BAC>
 A;Cross-references: EMBL:U41284; NID:G1679627; PIDN:AAB19185.1; PID:G1679628
 C;Genetics:
 A;Gene: GDB:COX5B
 A;Cross-references: GDB:127530; OMIM:123866
 A;Map position: 2cen-2q13
 A;Genome: nuclear
 C;Complex: part of a 13 chain complex spanning the inner mitochondrial membrane and con
 (see PIR:OTHUSA), Vb, V1a (see PIR:OGHU6A), V1b (see PIR:OGHU6B), V1c (see PIR:OGHU6C)
 m dimers within the mitochondrial inner-membrane
 C;Function:
 A;Description: the cytochrome-c oxidase complex catalyzes the oxidation of four molecu
 ns from the mitochondrial matrix producing two molecules of water and lowering the conc
 A;Note: the role of chain Vb is not clear
 C;Superfamily: mammalian cytochrome-c oxidase chain Vb
 C;Keywords: electron transfer; membrane-associated complex; mitochondrial inner membran
 F;1-31/Domain: transit peptide (mitochondrion) #status predicted <TNP>
 F;32-129/Product: cytochrome-c oxidase chain Vb #status predicted <MAT>
 F;91,93,113,116/Binding site: zinc (Cys) #status predicted

Query Match 55.1%; Score 59; DB 1; Length 129;
 Best Local Similarity 57.9%; Pred. No. 4;
 Matches 11; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

Qy 1 RGPFGAGAAASGPGGGAP 19
 ||||| | | | | |
 Db 20 RGPFGAAAMRSMASGGGVP 38

RESULT 6
 I48967
 brain-specific kinase - mouse
 C;Species: Mus musculus (house mouse)
 C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
 C;Accession: I48967
 R;Zhou, R.R.; Copeland, T.D.; Kromer, L.F.; Schulz, N.T.
 J. Neurosci. Res. 37, 129-143, 1994
 A;Title: Isolation and characterization of Bsk, a growth factor receptor-like tyrosine
 A;Reference number: I48967; MUID:94194581; PMID:8145300
 A;Accession: I48967
 A;Status: preliminary; translated from GB/EMBL/DBD
 A;Molecule type: mRNA
 A;Residues: 1-877 <RES>

A;Cross-references: UNIPROT:Q60629; EMBL:U07357; NID:9466369; PIDN:AAAL7038.1; PID:94663
C;Gene: Bsk
C;Superfamily: protein-tyrosine kinase, receptor type eph; fibronectin type III repeat h
C;Keywords: Atp; transmembrane protein
F;512-778/Domain: protein kinase homology <XIN>
F;520-528/Region: protein kinase ATP-binding motif
F;801-868/Domain: SAM homology <SAM>

Query Match 55.1%; Score 59; DB 2; Length 877;
Best Local Similarity 61.9%; Pred. No. 22;
Matches 13; Conservative 0; Mismatches 6; Indels 2; Gaps 1;

Qy 2 GPRGAGARASGPGG--APR 20
Db 5 GPRGAGHRRTQGRGGGDTPT 25
||||| | | | | |

RESULT 7
T21096
hypothetical protein F18H3.3b - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T21096
R;Coles, L.
submitted to the EMBL Data Library, July 1995
A;Reference number: Z19373
A;Accession: T21096
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-566 <WIL>
A;Cross-references: UNIPROT:Q19581; EMBL:Z50110; PIDN:CAA90446.1; GSPDB:GN00028; CESP:FI
A;Experimental source: clone F18H3
C;Genetics:
A;Gene: CESP:F18H3.3b
A;Map position: X
A;Introns: 111/1; 215/2; 469/3; 552/3
C;Superfamily: polyadenylate-binding protein; ribonucleoprotein repeat homology

Query Match 54.7%; Score 58.5; DB 2; Length 566;
Best Local Similarity 65.0%; Pred. No. 18;
Matches 13; Conservative 0; Mismatches 4; Indels 3; Gaps 1;

Qy 3 PRGAGARASGPG---GGAP 19
Db 530 PRPAGAPRVGGPGVQMGAP 549
||| | | | | |

RESULT 8
T21095
hypothetical protein F18H3.3a - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T21095
R;Coles, L.
submitted to the EMBL Data Library, July 1995
A;Reference number: Z19373
A;Accession: T21095
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-692 <WIL>
A;Cross-references: UNIPROT:Q19579; EMBL:Z50110; PIDN:CAA90444.1; GSPDB:GN00028; CESP:FI
A;Experimental source: clone F18H3
C;Genetics:
A;Gene: CESP:F18H3.3a
A;Map position: X
A;Introns: 111/1; 215/2; 469/3; 552/3
C;Superfamily: polyadenylate-binding protein; ribonucleoprotein repeat homology

Query Match 54.7%; Score 58.5; DB 2; Length 692;
Best Local Similarity 65.0%; Pred. No. 21;
Matches 13; Conservative 0; Mismatches 4; Indels 3; Gaps 1;

Qy 3 PRGAGARASGPG---GGAP 19
Db 530 PRPAGAPRVGGPGVQMGAP 549
||| | | | | |

RESULT 9
JC2254
cytochrome-c oxidase (EC 1.9.3.1) chain Vb precursor - rat
N;Alternate names: cytochrome-c oxidase (EC 1.9.3.1) chain V1a*
C;Species: Rattus norvegicus (Norway rat)
C;Date: 28-Oct-1994 #sequence_revision 26-May-1995 #text_change 09-Jul-2004
C;Accession: JC2254; J02255; S05318; S65375
R;Hoshinaga, H.; Amuro, N.; Goto, Y.; Okazaki, T.
J. Biochem. 115, 194-201, 1994
A;Title: Molecular cloning and characterization of the rat cytochrome c oxidase subunit
A;Reference number: JC2254; MUID:94266742; PMID:8206867
A;Accession: JC2254
A;Molecule type: mRNA
A;Residues: 1-129 <HOS>
A;Cross-references: UNIPROT:P12075; DBJ:D10952; NID:9493694; PIDN:BAA01744.1; PID:9493
A;Experimental source: liver
A;Accession: JC2255
A;Molecule type: DNA
A;Residues: 1-129 <HO2>
A;Cross-references: DBJ:D10951
A;Experimental source: lambda COXVb741
R;Goto, Y.; Amuro, N.; Okazaki, T.
Nucleic Acids Res. 17, 6389, 1989
A;Title: Nucleotide sequence of cDNA for rat liver and brain cytochrome c oxidase subunit
A;Reference number: S05318; MUID:89366688; PMID:2549512
A;Accession: S05318
A;Molecule type: mRNA
A;Residues: 31-129 <GOT>
A;Cross-references: EMBL:X14208
R;Schaeffer, H.; Noack, H.; Halangk, W.; Brandt, U.; von Jagow, G.
Eur. J. Biochem. 230, 235-241, 1995
A;Title: Cytochrome-c oxidase in developing rat heart. Enzymic properties and amino-ter-
A;Reference number: S65372; MUID:95324529; PMID:7601105
A;Accession: S65375
A;Molecule type: protein
A;Residues: 32-41 <SCH>
A;Experimental source: liver
C;Genetics:
A;Gene: COXVb-1
A;Introns: 35/1; 59/3; 93/1
A;Note: intronless gene COXVb-2 apparently a nonfunctional processed pseudogene
C;Superfamily: mammalian cytochrome-c oxidase chain Vb
C;Keywords: membrane-associated complex; mitochondrial inner membrane; mitochondrion; o
F;1-31/Domain: transit peptide (mitochondrion) #status predicted <TNP>
F;32-129/Product: cytochrome-c oxidase chain Vb #status predicted <MAT>

Query Match 53.3%; Score 57; DB 1; Length 129;
Best Local Similarity 55.6%; Pred. No. 8.2;
Matches 10; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

Qy 2 GPRGAGARASGPGGAP 19
Db 21 GPRGVAATRSASGGGVP 38
||| | | | | |

RESULT 10
T36273
hypothetical protein SCE68.23c - Streptomyces coelicolor
C;Species: Streptomyces coelicolor
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Accession: T36273
R;Murphy, L.; Harris, D.; James, K.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, June 1999
A;Reference number: Z21576
A;Accession: T36273
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-355 <MUR>

T46417
hypothetical protein DKFZp434K1323.1 - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 09-Jul-2004
C;Accession: T46417
R;Blum, H.; Bauersachs, S.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
submitted to the Protein Sequence Database, January 2000
A;Reference number: 223034
A;Accession: T46417
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-250 <AAA>
A;Cross-references: UNIPROT:Q9NSV7; EMBL:AL137714
A;Experimental source: adult testis; clone DKFZp434K1323
C;Genetics:
A;Note: DKFZp434K1323.1

Query Match 51.4%; Score 55; DB 2; Length 250;
Best Local Similarity 65.8%; Pred. No. 23;
Matches 11; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 RGRGAGAAARASGPGG 16
||| ||| ||| ||| |||
Db 9 RGRGGGGRRAALGPGG 24

Search completed: September 11, 2005, 01:43:53
Job time : 6.61905 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 11, 2005, 01:20:48 ; Search time 26.4762 Seconds
(without alignments)
386.822 Million cell updates/sec

Title: US-09-529-206E-4_COPY_43_62
Perfect score: 107
Sequence: 1 RGRGAGARASGPGGAPR 20

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt_03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	107	100.0	142	2 Q9NY13	Q9ny13 homo sapien
2	107	100.0	180	1 CTG1_HUMAN	P78358 homo sapien
3	99	92.5	210	1 CTG2_HUMAN	O75638 homo sapien
4	67	62.6	627	1 HYDL_STRCO	P42534 streptomyc
5	64	59.8	337	1 CT86_HUMAN	Q9bz19 homo sapien
6	62	57.9	301	2 Q8WSZ1	Q8wsz1 nephila cla
7	62	57.9	550	2 Q86P11	Q86p11 toxoplasma
8	62	57.9	1039	2 Q8S0W4	Q8s0w4 oryza sativ
9	62	57.9	1039	2 Q6F2Y0	Q6f2y0 oryza sativ
10	61.5	57.5	1953	2 Q9BI77	Q9bi77 nephila ina
11	60	56.1	450	1 A2AA_HUMAN	P08913 homo sapien
12	60	56.1	721	1 PUB2_RAT	Q99pf5 rattus norv
13	60	56.1	926	1 CEZ2_MOUSE	Q8r554 mus musculu
14	60	56.1	1005	1 EPA5_RAT	P54757 rattus norv
15	59	55.1	129	1 COXB_HUMAN	P10606 homo sapien
16	59	55.1	129	2 Q6FHJ9	Q6fhj9 homo sapien
17	59	55.1	129	2 Q6FH44	Q6fhm4 homo sapien
18	59	55.1	420	2 Q8CBY9	Q8cb9 mus musculu
19	59	55.1	538	2 Q8C278	Q8c278 mus musculu
20	59	55.1	681	2 Q8C276	Q8c276 mus musculu
21	59	55.1	819	2 Q6PFV6	Q6pfv6 mus musculu
22	59	55.1	877	1 EPA5_MOUSE	Q60629 mus musculu
23	58.5	54.7	563	2 Q9BIT5	Q9bit5 nephila ina
24	58.5	54.7	566	2 Q195B1	Q195b1 caenorhabdi
25	58.5	54.7	692	2 Q19579	Q19579 caenorhabdi
26	58	54.2	775	2 Q9F342	Q9f342 streptomyc
27	57	53.3	129	1 COXB_RAT	P12075 rattus norv
28	57	53.3	129	2 Q9DB81	Q9db81 mus musculu
29	57	53.3	329	2 Q6NLK4	Q6nlk4 drosophila
30	57	53.3	355	2 Q9WX09	Q9wx09 streptomyc
31	57	53.3	412	2 Q960D3	Q960d3 drosophila

32 57 53.3 437 2 Q8KUG4 Q8kug4 actinosynne
33 57 53.3 443 2 Q9VBX3 Q9vbx3 drosophila
34 57 53.3 457 2 Q94LK1 Q94lk1 oryza sativ
35 57 53.3 457 2 Q7G604 Q7g604 oryza sativ
36 57 53.3 644 2 Q688J5 Q688j5 oryza sativ
37 57 53.3 853 2 Q8VQZ0 Q8vqz0 myxococcus
38 57 53.3 857 2 Q85783 Q85783 myxococcus
39 57 53.3 866 1 SRC2_HUMAN Q96gp6 homo sapien
40 56 52.3 114 2 Q6B461 Q6b461 suid herpes
41 56 52.3 158 2 Q8C2G2 Q8c2g2 mus musculu
42 56 52.3 200 2 Q8W3A2 Q8w3a2 oryza sativ
43 56 52.3 256 2 Q96MK8 Q96mk8 homo sapien
44 56 52.3 478 2 Q82F52 Q82f52 streptomyc
45 56 52.3 520 2 Q7XLL8 Q7xll8 oryza sativ

ALIGNMENTS

RESULT 1

Q9NY13 PRELIMINARY; PRT; 142 AA.
AC Q9NY13;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DB Hypothetical protein LAGE-2 (Fragment).
GN Names=LAGE-2;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Lethe B.G.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ275978; CAB76945.1; -.
KW Hypothetical protein.
FT NON_TER 1
SQ SEQUENCE 142 AA; 13895 MW; 27EBE922AC4ACC7B CRC64;

Query Match 100.0%; Score 107; DB 2; Length 142;

Best Local Similarity 100.0%; Pred. No. 0.00032; Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGRGAGARASGPGGAPR 20

|||||
Db 17 RGRGAGARASGPGGAPR 36

RESULT 2

CTG1_HUMAN STANDARD; PRT; 180 AA.
ID CTG1_HUMAN
AC P78358;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Cancer/testis antigen 1B (Autoimmunogenic cancer/testis antigen NY-ESO-1).
DE ESO-1).
GN Name=CTAG1B; Synonyms=CTAG, CTAG1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RP MEDLINE=97203161; PubMed=9050879; DOI=10.1073/pnas.94.5.1914;
RA Chen Y.-T., Scanlan M.J., Sahin U., Tuerci O., Gure A.O., Tsang S.,
RA Williamson B., Stockert B., Pfleundschuh M., Old L.J.;
RT "A testicular antigen aberrantly expressed in human cancers detected
RT by autologous antibody screening.";
RL Proc. Natl. Acad. Sci. U.S.A. 94:1914-1918 (1997).
RN [2]

Query Match 92.5%; Score 99; DB 1; Length 210;
 Best Local Similarity 95.0%; Pred. No. 0.0032;
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RGPAGAGARASGPGGAPR 20
 |||||
 DB 43 RGPAGAGARASGPGGAPR 62
 |||||

RESULT 4
 HYDL_STRCO STANDARD; PRT; 627 AA.
 AC P42534; Q9S2L7;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Putative polyketide hydroxylase (EC 1.14.13.-) (Whie ORF VIII).
 GN OrderedLocusNames=SC05321; ORFNames=SC6G9.12C;
 OS Streptomyces coelicolor.
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC Streptomycineae; Streptomycetaceae; Streptomyces.
 OX NCBI_TaxID=1902;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=A3(2) / M145;
 RX MEDLINE=21996410; PubMed=12000953; DOI=10.1038/417141a;
 RA Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
 RA Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
 RA Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
 RA Cronin A., Fraser A., Gobie A., Hidalgo J., Hornsby T., Howarth S.,
 RA Huang C.-H., Kieser T., Larke L., Murphy L.D., Oliver K., O'Neill S.,
 RA Rabinowitz E., Rajandream M.A., Rutherford K.M., Rutter S.,
 RA Seeger K., Saunders D., Sharp S., Squares S., Taylor K.,
 RA Warren T., Wietzorrek A., Woodward J.R., Barrall B.G., Parkhill J.,
 RA Hopwood B.A.;
 RT "Complete genome sequence of the model actinomycete Streptomyces
 RT coelicolor A3(2).";
 RL Nature 417:141-147(2002).
 RN [2]
 RP SEQUENCE OF 1-255 FROM N.A.
 RC STRAIN=A3(2).
 RX MEDLINE=94075247; PubMed=8253693;
 RA Bianco G., Pereda A., Brian P., Mendez C., Chater K.F., Salas J.A.;
 RT "A hydroxylase-like gene product contributes to synthesis of a
 RT polyketide spore pigment in Streptomyces halstedii.";
 RL J. Bacteriol. 175:8043-8048(1993)
 CC -1- FUNCTION: Involved in developmentally regulated synthesis of a
 CC compound biosynthetically related to polyketide antibiotics which
 CC is essential for spore color in Streptococcus coelicolor.
 CC -1- COFACTOR: FAD (by similarity).
 CC -1- SIMILARITY: Belongs to the pheA/tfDB FAD monooxygenase family.
 CC
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 CC
 CC EMBL; AL393123; CAB94503.1; -
 CC EMBL; X74213; CAAS2289.1; -
 CC PIR; T35608; T35608.
 CC InterPro; IPR008160; Collagen.
 CC InterPro; IPR000733; Flav_monooxygenase.
 CC InterPro; IPR002938; Mox_FAD binding.
 CC InterPro; IPR003042; Rng_monooxygenase.
 CC Pfam; PF01494; FAD binding 3; 1.
 CC Pfam; PF01360; Monooxygenase; 1.
 CC PRINTS; PR00420; RNMNOXGNASE.
 CC Complete proteome; FAD; Flavoprotein; Oxidoreductase.
 KW NP_BIND 22 51 FAD (Potential).
 DR

FT NP_BIND 309 319 FAD (Potential).
 FT CONFLICT 60 60 R -> A (in Ref. 2).
 FT CONFLICT 145 145 L -> LH (in Ref. 2).
 FT CONFLICT 234 234 C -> S (in Ref. 2).
 SQ SEQUENCE 627 AA; 64557 MW; 746B84A2A9E9511C CRC64;

Query Match 62.6%; Score 67; DB 1; Length 627;
 Best Local Similarity 75.0%; Pred. No. 21;
 Matches 12; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 GPRGAGARASGPGGG 17
 |||||
 DB 447 GPRGAGAGGPGGG 462
 |||||

RESULT 5
 CT86_HUMAN STANDARD; PRT; 337 AA.
 AC Q9B219;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Hypothetical protein c20orf86.
 DE Name=C20orf86;
 GN Homo sapiens (Human).
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21638749; PubMed=11780052; DOI=10.1038/414865a;
 RA Deloukas P., Matthews L.H., Ashurst J.L., Burton J., Gilbert J.G.R.,
 RA Jones M., Stavridis G., Almeida J.P., Babbage A.K., Baguley C.L.,
 RA Bailey J., Barlow K.P., Bates K.N., Bead L.M., Beare D.M.,
 RA Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,
 RA Buck D., Burrill W.D., Butler A.P., Carder C., Carter N.P.,
 RA Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M.,
 RA Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,
 RA Coulson A., Coville G.J., Deadman R., Dhani P.D., Dunn M.,
 RA Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,
 RA Grahame D.V., Griffiths C., Griffiths M.N.D., Guilliam R., Hall R.E.,
 RA Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,
 RA Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,
 RA Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,
 RA Leharshaiho M.H., Leversha M.A., Lloyd C., Lloyd D.M., Lovell J.D.,
 RA Marsh V.L., Martin S.L., McConnachie L.J., McLay K., McMurray A.A.,
 RA Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,
 RA Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I.,
 RA Phillimore B.J.C.T., Prachalam S.R., Plumb R.W., Ramsay H.,
 RA Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Showkeen R., Sims S.,
 RA Suce C.D., Smith M.L., Soderlund C., Steward C.A., Sulston J.E.,
 RA Swann R.M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,
 RA Tracey A., Tromans A.C., Vaudin M., Wall M., Wallis J.M.,
 RA Whitehead S.L., Whitaker P., Willey D.L., Williams L., Williams S.A.,
 RA Wilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,
 RA Rogers J.;
 RT "The DNA sequence and comparative analysis of human chromosome 20.";
 RL Nature 414:865-871(2001).
 CC -1- SIMILARITY: Contains 2 ANK repeats.
 CC -1- SIMILARITY: Contains 1 ubiquitin-like domain.
 CC
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 CC EMBL; AL354776; CAC17565.2; -
 CC HSSP; P42771; 2A5E.
 CC Genew; HGNC:16217; C20orf86.
 CC InterPro; IPR002110; ANK.
 DR

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DR InterPro; IPR000626; Ubiquitin.
DR Pfam; PF00023; Ank; 3.
DR PRINTS; PRO1415; ANKYRIN.
DR SMART; SM00248; Ank; 2.
DR PROSITE; PS0297; ANK_REPEAT; 1.
DR PROSITE; PS00088; ANK_REPEAT; 2.
DR PROSITE; PS00299; UBIQUITIN_1; FALSE_NEG.
DR PROSITE; PS00053; UBIQUITIN_2; 1.
DR ANK repeat; Hypothetical protein; Polymorphism; Repeat.
FT DOMAIN 88 164 Ubiquitin-like.
FT REPEAT 211 241 ANK 1.
FT REPEAT 244 273 ANK 2.
FT VARIANT 287 287
FT SEQUENCE 337 AA; 36714 MW; EC8BA4AD414756CB CRC64;
Query Match 59.8%; Score 64; DB 1; Length 337;
Best Local Similarity 65.0%; Pred. No. 26;
Matches 13; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

Qy 1 RGRGAGAGARASGPGGAPR 20
| | | | | | | | | |
Db 3 RAAAGAGGARAAGTGGASR 22
| | | | | | | | | |

RESULT 6
Q8WSZ3 PRELIMINARY; PRT; 301 AA.
AC Q8WSZ3;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DE Dragline silk protein spidroin 2 (Fragment).
OS Nephila clavata (Joro spider).
OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Araneae;
OC Araneomorphae; Entelegynae; Aranezoidea; Tetragnathidae; Nephila.
OX NCBI_TaxID=70342;
RN [1]
RP SEQUENCE FROM N.A.
RA Ma H.W., Zhang L.S., Lu Y.M., Liu Z.S., Zhang Y.J.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF441245; AAL32472.1; -.
FT NON_TER 1 1
FT NON_TER 301 301
FT SEQUENCE 301 AA; 25396 MW; 8C69428B5684ED74 CRC64;
Query Match 57.9%; Score 62; DB 2; Length 301;
Best Local Similarity 66.7%; Pred. No. 38;
Matches 12; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 2 GPRGAGARASGPGGAP 19
| | | | | | | | | |
Db 130 GPGGAAAAAAGPGGYG 147
| | | | | | | | | |

RESULT 7
Q86P11 PRELIMINARY; PRT; 550 AA.
AC Q86P11;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Jip2.
OS Toxoplasma gondii.
OC Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida; Sarcocystidae;
OC Toxoplasma.
OX NCBI_TaxID=5811;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=RH;
RA Jiang L., Shu H., Luo S., Wu X., Cai L., Wang D., Zeng Q.;
RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY208675; AAO43429.1; -.
SQ SEQUENCE 550 AA; 57890 MW; 18C71B4974BF0F34 CRC64;
Query Match 57.9%; Score 62; DB 2; Length 550;
Best Local Similarity 63.2%; Pred. No. 65;
Matches 12; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 2 GPRGAGARASGPGGAPR 20
| | | | | | | | | |
Db 524 GPGGAGAAQADGAGGPR 542
| | | | | | | | | |

RESULT 8
Q8SOW4 PRELIMINARY; PRT; 1039 AA.
ID Q8SOW4;
AC Q8SOW4;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE QJ1014 G12.10 protein.
GN Name=QJ1014_G12.10;
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=12447438; DOI=10.1038/nature01184;
RA Sasaki T., Matsumoto T., Yamamoto K., Sakata K., Baba T., Katayose Y.,
RA Wu J., Niimura Y., Cheng Z., Nagamura Y., Antonio B.A., Kanamori H.,
RA Hosokawa S., Masukawa M., Arikawa K., Chiden Y., Hayashi M.,
RA Okamoto M., Ando T., Aoki H., Arita K., Hamada M., Harada C.,
RA Hijishita S., Honda M., Ichikawa Y., Idonuma A., Iijima M., Ikeda M.,
RA Ikono M., Itoh S., Itoh T., Itoh Y., Iwabuchi A., Kamiya K.,
RA Karasawa W., Katagiri S., Kikuta A., Kobayashi N., Kono I.,
RA Machita K., Maehara T., Mizuno H., Mizubayashi T., Mukai Y.,
RA Nagaaki H., Nakaehima M., Nakama Y., Nakamichi Y., Nakamura M.,
RA Namiki N., Negishi M., Ohta I., Ono N., Saji S., Sakai K., Shibata M.,
RA Shimokawa T., Shomura A., Song J., Takazaki Y., Terasawa K., Tsuji K.,
RA Waki K., Yamagata H., Yamane H., Yoshiki S., Yoshihara K., Yukawa K.,
RA Zhong H., Iwama H., Endo T., Ito H., Hahn J.H., Kim H.I., Eun M.Y.,
RA Yano M., Jiang J., Gojobori T.;
RT "The genome sequence and structure of rice chromosome 1.";
RL Nature 420:312-316(2002).
DR EMBL; AP003372; BAB89076.1; -.
DR Gramene; Q8SOW4; -.
DR InterPro; IPR011038; Calycin.
DR InterPro; IPR007228; DUF390.
DR InterPro; IPR007321; Transposase_28.
DR Pfam; PF04094; DUF390; 1.
DR Pfam; PF04195; Transposase_28; 1.
SQ SEQUENCE 1039 AA; 112082 MW; A9A60FD3487B5DFD CRC64;
Query Match 57.9%; Score 62; DB 2; Length 1039;
Best Local Similarity 73.7%; Pred. No. 11e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 2; Gaps 1;

Qy 3 PRGAGARASG--PGGAP 19
| | | | | | | | | |
Db 363 PRGGGAARASSRRPEGAP 381
| | | | | | | | | |

RESULT 9
Q6FY0 PRELIMINARY; PRT; 1039 AA.
ID Q6FY0;
AC Q6FY0;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Hypothetical protein OSJNBa0038E22.10.
GN Name=OSJNBa0038E22.10;
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

```

OC	Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC	Ehrhartoidae; Oryzae; Oryza.
OX	NCBI_TaxID=39947;
RN	[1]
RP	SEQUENCE FROM N.A.
RA	Chow T.-Y., Heing Y.-I., Chen C.-S., Chen H.-H., Liu S.-M.,
RA	Chao Y.-T., Chang S.-J., Chen H.-C., Chen S.-K., Chen T.-R.,
RA	Chen Y.-L., Cheng C.-H., Chung C.-I., Han S.-Y., Hsiao S.-H.,
RA	Hsiung J.-N., Hsu C.-H., Huang J.-J., Kau P.-I., Lee M.-C.,
RA	Li Y.-F., Lin S.-J., Lin Y.-C., Wu S.-W., Yu C.-Y., Yu S.-W.,
RA	Wu H.-P., Shaw J.-F., *McCombie W.R., *Spiegel L., *de la Bastide M.,
RA	*Zutavern T., *Muller S., *Nascimento L., *Balijs V., *Bell M.,
RA	*Willer B., *Katzenberger F., *Andrade M.V., *Dike S.,
RA	*O'Shaughnessy A., *Palmer L., *Dedhia N.;
RL	Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
DR	EMBL; AC132484; AA73650.1; -
DR	InterPro; IPR011038; Calycin.
DR	InterPro; IPR007228; DUF390.
DR	InterPro; IPR007321; Transposase_28.
DR	Pfam; PF04094; DUF390; 1.
DR	Pfam; PF04195; Transposase_28; 1.
KW	Hypothetical protein.
SQ	SEQUENCE 1039 AA; 111214 MW; 856219894B2FB717 CRC64;
	Query Match 57.9%; Score 62; DB 2; Length 1039;
	Best Local Similarity 73.7%; Pred. No. 1.1e+02;
	Matches 14; Conservative 0; Mismatches 3; Indels 2; Gaps 1;
QY	3 PRGGAARASG--PGGGAP 19
Dd	322 PRGGAARASRRPEGAAP 340
RESULT 10	
QBIT7	PRELIMINARY; PRT; 1953 AA.
ID	QBIT7;
AC	QBIT7;
DT	01-JUN-2001 (TrEMBLrel. 17, Created)
DT	01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DE	01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE	Major ampullate spiderin 2-like protein (Fragment).
OS	Nephila inaurata madagascariensis.
OC	Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Araneae;
OC	Araconomorphae; Entelegynae; Araneioidea; Tetragnathidae; Nephila.
OX	NCBI_TaxID=115969;
RN	[1]
RP	SEQUENCE FROM N.A.
RA	MEDLINE=J1179804; PubMed=11283372; DOI=10.1126/science.1057561;
RA	Gatesy J.E., Hayashi C., Motriuk D., Woods J., Lewis R.;
RL	Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR	EMBL; AF350276; AAK30605.1; -
FT	NON_TER 1
FT	NON_TER 1953
FT	NON_TER 1953
SQ	SEQUENCE 1953 AA; 159383 MW; C82B4DACD043C3BD CRC64;
	Query Match 57.5%; Score 61.5; DB 2; Length 1953;
	Best Local Similarity 68.4%; Pred. No. 2.2e+02;
	Matches 13; Conservative 2; Mismatches 3; Indels 1; Gaps 1;
QY	1 RGRPGAGARASFGGGAP 19 : :
Dd	152 QGRPGCAA-AAGPGGYGP 169 : :
RESULT 11	
A2AA_HUMAN	STANDARD; PRT; 450 AA.
ID	A2AA_HUMAN
AC	QBIT7;
DT	01-NOV-1988 (Rel. 09, Created)
DT	01-FEB-1996 (Rel. 33, Last sequence update)
DT	25-OCT-2004 (Rel. 45, Last annotation update)
DE	Alpha-2A adrenergic receptor (Alpha-2A adrenoceptor) (Alpha-2A
DE	adrenoreceptor) (Alpha-2AAR subtype C10).
OS	Name ADRA2A; Synonyms=ADRA2R, ADRAR;
OS	Homo sapiens (Human).
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OX	NCBI_TaxID=9606;
RN	[1]
RP	SEQUENCE FROM N.A.
RA	MEDLINE=89308571; PubMed=2568356;
RA	Fraser C.M., Arakawa S., McCombie W.R., Venter J.C.;
RL	"Cloning, sequence analysis, and permanent expression of a human alpha
RL	2-adrenergic receptor in Chinese hamster ovary cells. Evidence for
RL	attenuation pathways of receptor coupling to adenylate cyclase
RL	J. Biol. Chem. 264:11754-11761(1989).
RN	[2]
RP	SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC	TISSUE=Platelet;
RX	MEDLINE=88042789; PubMed=2823383;
RA	Koblika B.K., Matsui H., Kobilka T.S., Yang-Feng T.L., Francke U.,
RA	Caron M.G., Lefkowitz R.J., Regan J.W.;
RL	"Cloning, sequencing, and expression of the gene coding for the human
RL	platelet alpha 2-adrenergic receptor.";
RL	Science 238:650-656(1987).
RN	[3]
RP	REVISIONS TO 333-365.
RX	MEDLINE=91009167; PubMed=2170371;
RA	Guyver C.A., Horstman D.A., Wilson A.L., Clark J.D., Kragoe B.J. Jr.,
RA	Limbird L.E.;
RL	"Cloning, sequencing, and expression of the gene encoding the porcine
RL	alpha 2-adrenergic receptor. Allosteric modulation by Na+, H+, and
RL	amiloride analogs.";
RL	J. Biol. Chem. 265:17307-17317(1990).
RN	[4]
RP	SEQUENCE FROM N.A.
RA	Castellano M., Giacche' M., Rossi F., Rivadosi F., Perani C.,
RA	Beschi M., Agabiti Rosei E.;
RL	"A search for genetic variability in the human alpha-2 adrenergic
RL	receptor on chromosome 10.";
RL	Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
RN	[5]
RP	SEQUENCE FROM N.A., AND VARIANT LYS-251.
RX	PubMed=10948191; DOI=10.1074/jbc.M004550200;
RA	Small K.M., Forbes S.L., Brown K.M., Liggett S.B.;
RL	"An Asn to Lys polymorphism in the third intracellular loop of the
RL	human alpha 2A-adrenergic receptor imparts enhanced agonist-promoted
RL	GI coupling.";
RL	J. Biol. Chem. 275:38518-38523(2000).
RN	[6]
RP	SEQUENCE FROM N.A.
RA	Mao Z.-M., Tang K., Li B.-M., Jing N.-H.;
RL	"Cloning and expression of human alpha-2A adrenergic receptor in SY5Y
RL	cells.";
RL	Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
RN	[7]
RP	SEQUENCE FROM N.A.
RA	Liu L., Yuan L.;
RL	"Human alpha-2A adrenergic receptor gene and the genotype of -1296
RL	nucleotide and motility sickness.";
RL	Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
RN	[8]
RP	SEQUENCE FROM N.A.
RC	TISSUE=PNS;
RX	MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA	Klausner R.D., Collins F.S., Wagner L., Shenmen J.G., Schuler G.D.,
RA	Altschul S.F., Zeeberg K., B

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Uedin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalusz D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 [9]
 RN MUTAGENESIS OF PHE-412.
 RP MEDLINE=91332079; PubMed=1678390;
 RX Suryaaryana S., Daunt D.A., von Zastrow M., Kobilka B.K.;
 RA "A point mutation in the seventh hydrophobic domain of the alpha 2
 RA adrenergic receptor increases its affinity for a family of beta
 RT receptor antagonists.";
 RL J. Biol. Chem. 266:15488-15492 (1991).
 [10]
 RN MUTAGENESIS OF ASPARTIC ACID AND SERINE RESIDUES.
 RP MEDLINE=91342598; PubMed=1678850;
 RX Wang C.-D., Buck M.A., Fraser C.M.;
 RA "Site-directed mutagenesis of alpha 2a-adrenergic receptors:
 RT Identification of amino acids involved in ligand binding and receptor
 RT activation by agonists.";
 RL Mol. Pharmacol. 40:168-179 (1991).
 CC -!- FUNCTION: Alpha-2 adrenergic receptors mediate the catecholamine-
 CC induced inhibition of adenylate cyclase through the action of G
 CC proteins. The rank order of potency for agonists of this receptor
 CC is oxymetazoline > clonidine > epinephrine > norepinephrine >
 CC phenylephrine > dopamine > p-synephrine > p-tyramine > serotonin =
 CC p-ocetamine. For antagonists, the rank order is yohimbine >
 CC phentolamine = mianserin > chlorpromazine = spiperone = prazosin
 CC > propranolol > alprenolol = pindolol.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
 CC
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 CC
 CC EMBL; M23533; AAA51665.1; -;
 CC EMBL; M18415; AAA51664.1; -;
 CC EMBL; AF262016; AAG00447.2; -;
 CC EMBL; AF281308; AAF91441.1; -;
 CC EMBL; AF316894; AAK01634.1; -;
 CC EMBL; AF284095; AAK26743.1; -;
 CC EMBL; AY032736; AAK51162.1; -;
 CC EMBL; BC050414; AAHS0414.2; -;
 CC PIR; A34169; A34169.
 CC PDB; 1HLL; NMR; A=118-149.
 CC PDB; 1HO9; NMR; A=118-149.
 CC PDB; 1HOD; NMR; A=118-149.
 CC PDB; 1HOF; NMR; A=118-149.
 CC Genew; HGNC:281; ADRA2A.
 CC MIM; 104210; -;
 CC GO; GO:0005887; C:integral to plasma membrane; TAS.
 CC GO; GO:0004938; F:alpha2-adrenergic receptor activity; TAS.
 CC GO; GO:0015459; F:potassium channel regulator activity; TAS.
 CC GO; GO:0030036; P:actin cytoskeleton organization and biogenesis; TAS.
 CC GO; GO:0000187; P:activation of WAPK; TAS.
 CC GO; GO:0006928; P:cell motility; TAS.
 CC GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; TAS.

DR GO; GO:0007194; P:negative regulation of adenylate cyclase ac. .; TAS.
 DR GO; GO:0008284; P:positive regulation of cell proliferation; TAS.
 DR GO; GO:0007265; P:RAS protein signal transduction; TAS.
 DR GO; GO:0007266; P:Rho protein signal transduction; TAS.
 DR GO; GO:0007165; P:signal transduction; TAS.
 DR InterPro; IPR001946; A:receptorA2Aa.
 DR InterPro; IPR000276; GPCR_Rhodopsn.
 DR Pfam; PF00001; 7tm1; 1.
 DR PRINTS; PR00558; ADRENRGA2AR.
 DR PRINTS; PR00237; GPCRRHODOPSN.
 DR PROSITE; PS00237; G-PROTEIN_RECEP_F1_1; 1.
 DR PROSITE; PS00262; G-PROTEIN_RECEP_F1_2; 1.
 DR 3D-structure; Direct protein sequencing; G-protein coupled receptor;
 KW Glycoprotein; Lipoprotein; Multigene family; Palmitate;
 KW Phosphorylation; Polymorphism; Transmembrane.
 FT DOMAIN 1 33 Extracellular (Potential).
 FT TRANSMEM 34 59 1 (Potential).
 FT DOMAIN 60 70 Cytoplasmic (Potential).
 FT TRANSMEM 71 96 2 (Potential).
 FT DOMAIN 97 106 Extracellular (Potential).
 FT TRANSMEM 107 129 3 (Potential).
 FT DOMAIN 130 149 Cytoplasmic (Potential).
 FT TRANSMEM 150 173 4 (Potential).
 FT DOMAIN 174 192 Extracellular (Potential).
 FT TRANSMEM 193 217 5 (Potential).
 FT DOMAIN 218 374 Cytoplasmic (Potential).
 FT TRANSMEM 375 399 6 (Potential).
 FT DOMAIN 400 406 Extracellular (Potential).
 FT TRANSMEM 407 430 7 (Potential).
 FT DOMAIN 431 450 Cytoplasmic (Potential).
 FT CARBOHYD 10 10 N-linked (GlcNAc. .) (Potential).
 FT CARBOHYD 14 14 By similarity.
 FT LIPID 106 188 S-palmitoyl cysteine (By similarity).
 FT SITE 442 442 Implicated in ligand binding.
 FT SITE 113 113 Implicated in catechol agonist binding
 FT SITE 200 200 and receptor activation.
 FT SITE 204 204 Implicated in catechol agonist binding
 FT VARIANT 251 251 and receptor activation.
 FT MUTAGEN 79 N -> K (rare polymorphism; frequency in
 FT CAUCASIANS 0.004 and in African-Americans
 FT 0.05; 40% increase in agonist-promoted Gi
 FT coupling; dbSNP:1800035).
 FT /FTID-VAR 014957
 FT D-N: No change in binding affinity.
 FT eliminates guanine nucleotide-sensitive
 FT agonist binding.
 FT D-N: No binding to yohimbine. Increase
 FT in adenylate cyclase activity.
 FT D-N: Lower affinity for agonists.
 FT Eliminates guanine nucleotide-sensitive
 FT agonist binding.
 FT S-A: Lower affinity for agonists. No
 FT
 Query Match 56.1%; Score 60; DB 1; Length 450;
 Best Local Similarity 63.6%; Pred. No. 89;
 Matches 14; Conservative 0; Mismatches 6; Indels 2; Gaps 1;
 Qy 1 RGPGRGAGARAS--GPGGGAPR 20
 ||||| ||||| ||||| |||||
 Db 313 RGPGRGKARASQVKGDSLPR 334
 RESULT 12
 FUB2 RAT
 ID_FUB2 RAT STANDARD; PRT; 721 AA.
 AC Q9SPF5;
 DT 10-OCT-2003 (Rel. 42, Created)
 DT 10-OCT-2003 (Rel. 42, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Far upstream element binding protein 2 (FUSE binding protein 2) (KH
 DE type splicing regulatory protein) (KSRP) (MAP2 RNA trans-acting
 DE protein 1) (MARTAL).

GN Name=Pubp2; Synonyms=Khsrp;
 OS Rattus norvegicus (Rat).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 CC NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A., SEQUENCE OF 73-87; 89-108 AND 475-486, SUBCELLULAR
 RP LOCATION, AND FUNCTION.
 RC TISSUE=Brain;
 RX MEDLINE=22246918; PubMed=12358751;
 RA Rehbein M., Wege K., Buck F., Schweizer M., Richter D., Kindler S.;
 RT "Molecular characterization of MARTAL, a protein interacting with the
 RT dendritic targeting element of MAP2 mRNAs.";
 RL J. Neurochem. 82:1039-1046(2002).
 CC -!- FUNCTION: Part of a ternary complex that binds to the downstream
 CC control sequence (DCS) of the pre-mRNA. Mediates exon inclusion in
 CC transcripts that are subject to tissue-specific alternative
 CC splicing. May interact with single-stranded DNA from the far-
 CC upstream element (FUSE). May activate gene expression (By
 CC similarity). Binds to the dendritic targeting element and may play
 CC a role in mRNA trafficking.
 CC -!- SUBUNIT: Part of a ternary complex containing FUBP2, PTBP1, PTBP2
 CC and HNRPH1 (By similarity).
 CC -!- SUBCELLULAR LOCATION: Nuclear. A small proportion is also found in
 CC the cytoplasm of neuronal cell bodies and dendrites.
 CC -!- SIMILARITY: Contains 4 KH domains.
 CC
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 CC -----
 DR EMBL; AF308818; AAC59811.1; -.
 DR HSP; Q96AE4; IJ4W.
 DR GO; GO:0005515; F:protein binding; IPI.
 DR InterPro; IPR004087; KH.
 DR InterPro; IPR004088; KH_type_1.
 DR Pfam; PF00013; KH; 4.
 DR SMART; SM00322; KH; 4.
 DR PROSITE; PS00084; KH_TYPE_1; 4.
 KW Direct protein sequencing; DNA-binding; mRNA processing;
 KW mRNA splicing; mRNA transport; Nuclear protein; Repeat; RNA-binding;
 KW Trans-acting factor; Transcription regulation; Transport.
 FT DOMAIN 145 209 KH 1.
 FT DOMAIN 234 300 KH 2.
 FT DOMAIN 323 387 KH 3.
 FT DOMAIN 425 492 KH 4.
 FT DOMAIN 572 685 4 X 12 AA imperfect repeats.
 FT REPEAT 572 583 1.
 FT REPEAT 618 629 2.
 FT REPEAT 644 655 3.
 FT REPEAT 674 685 4.
 FT DOMAIN 7 68 Gly/Pro-rich.
 FT DOMAIN 69 498 Gly-rich.
 FT DOMAIN 499 613 Ala/Gly/Pro-rich.
 FT SEQUENCE 721 AA; 74226 MW; 482C7A765C60EE4A CRC64;
 Query Match 56.1%; Score 60; DB 1; Length 721;
 Best Local Similarity 61.1%; Pred. No. 1.3e+02;
 Matches 11; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
 QY 2 GPRGAGARASGGGGAP 19
 DB 33 GPPGAGDRGGGGGGGP 50
 RESULT 13
 CE22_MOUSE
 ID _CB22_MOUSE STANDARD; PRT; 926 AA.
 AC QBR554;

DT 25-OCT-2004 (Rel. 45, Created)
 DT 25-OCT-2004 (Rel. 45, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Zinc finger A20 domain containing protein ? (EC 3.-.-.-) (Zinc finger
 DE protein Cezanne 2).
 OS Mus musculus (Mouse).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 CC NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RP STRAIN=CS7BL/6;
 RA Evans P.C., Coadwell W.J., Kilshaw P.J.;
 RT "Isolation of a novel murine gene, Cezanne 2.";
 RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: Has deubiquitinating activity that is directed towards
 CC lys-48 or lys-63-linked polyubiquitin chains. Hydrolyzes both
 CC linear and branched forms of polyubiquitin (By similarity).
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic and nuclear (By similarity).
 CC -!- SIMILARITY: Belongs to the peptidase C64 family.
 CC -!- SIMILARITY: Contains 1 A20-type zinc finger.
 CC -!- SIMILARITY: Contains 1 OTU domain.
 CC
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 CC -----
 DR EMBL; AJ430384; CAD23048.1; -.
 DR MEROPS; C64.002; -.
 DR MGD; MGI:2158505; AJ430384.
 DR InterPro; IPR003323; OTU.
 DR Pfam; PF02338; OTU; 1.
 DR PROSITE; PS0802; OTU; 1.
 DR Hydrolase; Nuclear protein; Thiol protease; Ub1 conjugation pathway;
 KW Zinc-finger.
 FT DOMAIN 170 413 TRAF-binding (By similarity).
 FT DOMAIN 185 452 Catalytic (By similarity).
 FT DOMAIN 201 377 OTU.
 FT DOMAIN 497 512 Nuclear localization signal (Potential).
 FT DOMAIN 441 926 Ubiquitin-binding (By similarity).
 FT ZN_FING 890 910 A20-type (By similarity).
 FT ACT_SITE 209 209 By similarity.
 FT ACT_SITE 212 212 By similarity.
 FT ACT_SITE 370 370 By similarity.
 FT SEQUENCE 926 AA; 100796 MW; 4D6BD05A0410BED9 CRC64;
 Query Match 56.1%; Score 60; DB 1; Length 926;
 Best Local Similarity 60.0%; Pred. No. 1.7e+02;
 Matches 12; Conservative 1; Mismatches 7; Indels 0; Gaps 0;
 QY 1 RGPRGAGARASGGGGAPR 20
 DB 739 RAARAAGGAASPGGGGARR 758
 RESULT 14
 EPAS_RAT
 ID EPAS5 RAT STANDARD; PRT; 1005 AA.
 AC P54757;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Ephrin type-A receptor 5 precursor (EC 2.7.1.112) (Tyrosine-protein
 DE kinase receptor EHK-1) (SPH homology kinase-1).
 GN Name=EphA5; Synonyms=Ehk-1, Ekhl;
 OS Rattus norvegicus (Rat).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 CC NCBI_TaxID=10116;

RN [1]
 RP SEQUENCE FROM N.A. (ISOFORMS 1; 2; 3; 4 AND 5).
 RC STRAIN=Sprague-Dawley; TISSUE=Brain;
 RX MEDLINE=94067777; PubMed=7504232;
 RA Maisonnier P.C., Barreuxeta N.X., Yancopoulos G.D.;
 RT "Ehk-1 and Ehk-2: two novel members of the Eph receptor-like tyrosine
 RL kinase family with distinctive structures and neuronal expression.";
 ONCogene 8:3277-3288(1993).
 [2]
 RN SEQUENCE FROM N.A. (ISOFORM 6).
 RP STRAIN=Sprague-Dawley; TISSUE=Brain;
 RX MEDLINE=95266467; PubMed=7898646; DOI=10.1016/0306-4522(94)90014-0;
 RA Taylor V., Miescher G.C., Pfarr S., Honegger P., Breitschopf H.,
 RA Lassmann H., Steck A.J.;
 RT "Expression and developmental regulation of Ehk-1, a neuronal Elk-like
 RL receptor tyrosine kinase in brain.";
 Neuroscience 63:163-178(1994).
 CC -1- FUNCTION: Receptor for members of the ephrin-A family. Binds to
 CC ephrin-A1, -A2, -A3, -A4 and -A5.
 CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
 CC tyrosine phosphate.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event-Alternative splicing; Named isoforms=6;
 CC Name=1;
 CC IsoId=P54757-1; Sequence=Displayed;
 CC Name=2;
 CC IsoId=P54757-2; Sequence=VSP_003001;
 CC Name=3;
 CC IsoId=P54757-3; Sequence=VSP_003002;
 CC Name=4;
 CC IsoId=P54757-4; Sequence=VSP_003002, VSP_003003;
 CC Name=5;
 CC IsoId=P54757-5; Sequence=VSP_003001, VSP_003002, VSP_003003;
 CC Name=6;
 CC IsoId=P54757-6; Sequence=VSP_003000, VSP_003002;
 CC TISSUE SPECIFICITY: Almost exclusively expressed in the nervous
 CC system. Predominantly expressed in neurons.
 CC -1- SIMILARITY: Belongs to the Tyr protein kinase family. Ephrin
 CC receptor subfamily.
 CC -1- SIMILARITY: Contains 2 fibronectin type III domains.
 CC -1- SIMILARITY: Contains 1 sterile alpha motif (SAM) domain.
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 CC -----
 CC EMBL: X78689; CAA55357.1; --
 CC PIR: S49015; S49015.
 CC PIR: S51603; S51603.
 CC HSP: P54763; LUPA.
 CC InterPro: IPR006209; EGF like.
 CC InterPro: IPR001090; Ephrin receptor.
 CC InterPro: IPR003961; FN III.
 CC InterPro: IPR008957; FN-III-like.
 CC InterPro: IPR003962; FNIII subd.
 CC InterPro: IPR008979; Gal_bind_like.
 CC InterPro: IPR009030; Grow_fac_recept.
 CC InterPro: IPR011009; Kinase like.
 CC InterPro: IPR000719; Prot_kinase.
 CC InterPro: IPR001660; SAM.
 CC InterPro: IPR001245; Tyr_kinase.
 CC InterPro: IPR008266; Tyr_kinase_AS.
 CC InterPro: IPR001426; Ykase_receptorV.
 CC Pfam: PF01404; Ephrin_lbd; 1.
 CC Pfam: PF00041; fn3; 2.
 CC Pfam: PF00069; Pkinase; 1.
 CC Pfam: PF00536; SAM; 1.
 CC PRINTS; PR00014; FNTYPEIII.

DR PRINTS; PR00109; TYRKINASE.
 DR ProDom; PD001495; Ephrin_receptor; 1.
 DR ProDom; PD000001; Prot_kinase; 1.
 DR SMART; SM00615; EPH_lbd; 1.
 DR SMART; SM00060; FN3; 2.
 DR SMART; SM00219; TYKc; 1.
 DR PROSITE; PS01186; EGF_2; UNKNOWN_1.
 DR PROSITE; PS00853; FN3; 2.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; FALSE_NEG.
 DR PROSITE; PS0011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
 DR PROSITE; PS00790; RECEPTOR_TYR_KIN_V_1; 1.
 DR PROSITE; PS00791; RECEPTOR_TYR_KIN_V_2; 1.
 DR PROSITE; PS00105; SAM_DOMAIN; 1.
 KW Alternative splicing; ATP-binding; Glycoprotein; Phosphorylation;
 KW Receptor; Repeat; Signal; Transferase; Transmembrane;
 KW Tyrosine-protein kinase.
 FT SIGNAL 1 26 By similarity.
 FT CHAIN 27 1005 Ephrin type-A receptor 5.
 FT DOMAIN 27 575 Extracellular (Potential).
 FT TRANSMEM 576 596 Potential.
 FT DOMAIN 597 1005 Cytoplasmic (Potential).
 FT DOMAIN 222 356 Cys-rich.
 FT DOMAIN 359 461 Fibronectin type-III 1.
 FT DOMAIN 471 561 Fibronectin type-III 2.
 FT DOMAIN 677 938 Protein kinase.
 FT DOMAIN 967 1005 SAM.
 FT NP_BIND 683 691 ATP (By similarity).
 FT BINDING 709 709 ATP (By similarity).
 FT ACT_SITE 802 802 Phosphotyrosine (by autocatalysis) (By
 FT MOD_RES 652 652 similarity).
 FT MOD_RES 658 658 Phosphotyrosine (by autocatalysis) (By
 FT MOD_RES 835 835 similarity).
 FT MOD_RES 835 835 Phosphotyrosine (by autocatalysis) (By
 FT MOD_RES 984 984 similarity).
 FT CARBOHYD 266 266 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 301 301 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 371 371 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 425 425 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 438 438 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 463 463 N-linked (GlcNAc...) (Potential).
 FT VARSPLIC 10 20 GRRTGGRGG -> DADGPRAGASWCHARR (in
 FT isoform 6).
 FT /FTId=VSP_003000.
 FT VARSPLIC 306 357 VCRPGFKASPHSQTKSCPPHSYTHEASTSCVCKDYFR
 FT RESDPTMACT -> G (in isoform 2 and
 FT isoform 5).
 FT /FTId=VSP_003001.
 FT VARSPLIC 358 470 RPPSAPRNAISNVNSETSFLWIPPADTGGKDVSYILCK
 FT KCMHAGVCECGHVRYPQQIGLKNYSVMADPLAHNTY
 FT TPEIEAVGVSDLSPTGTRQYVNVTTNQAA -> T (in
 FT isoform 3, isoform 4, isoform 5 and
 FT isoform 6).
 FT /FTId=VSP_003002.
 FT VARSPLIC 597 621 SGSCCGCGGRASSLCAVAHPSLIW -> R (in
 FT isoform 4 and isoform 5).
 FT /FTId=VSP_003003.
 FT CONFLICT 170 170 D -> E (in Ref. 2).
 FT CONFLICT 566 566 G -> A (in Ref. 2).
 FT CONFLICT 578 578 G -> A (in Ref. 2).
 FT CONFLICT 669 669 G -> A (in Ref. 2).
 FT CONFLICT 708 708 T -> I (in Ref. 2).
 FT CONFLICT 979 979 T -> I (in Ref. 2).
 SQ SEQUENCE 1005 AA; 111007 MW; 1AED42C99693C574 CRC64;
 Query Match 56.1%; Score 60; DB 1; Length 1005;
 Best Local Similarity 61.9%; Pred.No. 1.8e+02;
 Matches 13; Conservative 0; Mismatches 6; Indels 2; Gaps 1;
 QY 2 GPRGAGAARASGPGGG--APR 20


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Db 5 GPRGAGRRRTQGRGGGDTPT 25
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RESULT 15
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ID COXB_HUMAN STANDARD; PRT; 129 AA.
AC P10606; Q96J18;
DT 01-JUL-1989 (Rel. 11, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Cytochrome c oxidase polypeptide Vb, mitochondrial precursor
DE (EC 1.9.3.1).
GN Name=COX5B;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
[1]
SEQUENCE FROM N.A.
RX MEDLINE=88284368; PubMed=2840351; DOI=10.1016/0378-1119(88)90411-8;
RA Zeviani M., Sakoda S., Sherbany A., Nakase H., Rizzuto R.,
RA Samitt C.E., Dimauro S., Schon E.A.;
RT "Sequence of cDNAs encoding subunit Vb of human and bovine cytochrome
RT c oxidase."
RT Gene 65:1-11(1988).
RL [2]
SEQUENCE FROM N.A.
RX MEDLINE=91257815; PubMed=1646156;
RA Lomax M.I., Hsieh C.L., Darras B.T., Francke U.;
RT "Structure of the human cytochrome c oxidase subunit Vb gene and
RT chromosomal mapping of the coding gene and of seven pseudogenes."
RL Genomics 10:1-9(1991).
[3]
SEQUENCE FROM N.A.
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uedin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywicki M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[4]
SEQUENCE OF 32-44.
RX MEDLINE=94147969; PubMed=8313870;
RA Hughes G.J., Frutiger S., Paquet N., Pasquali C., Sanchez J.-C.,
RA Tissot J.-D., Bairoch A., Appel R.D., Hochstrasser D.F.;
RT "Human liver protein map: update 1993."
RL Electrophoresis 14:1216-1222(1993)
CC -!- FUNCTION: This protein is one of the nuclear-coded polypeptide
CC chains of cytochrome c oxidase, the terminal oxidase in
CC mitochondrial electron transport.
CC -!- CATALYTIC ACTIVITY: 4 ferrocycytochrome c + O(2) = 4 ferricytochrome
CC c + 2 H(2)O.
CC -!- SUBCELLULAR LOCATION: Mitochondrial inner membrane.
CC -!- SIMILARITY: Belongs to the cytochrome c oxidase Vb family.
```

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CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; M59250; AAA52060.1; -.
CC EMBL; M19961; AAA52061.1; -.
CC EMBL; BC006229; AAH06229.1; -.
CC FIR; JT0324; OTHUSB.
CC SWISS-2DPAGE; P10606; HUMAN.
CC Genew; HGNC:2269; COX5B.
CC H-InvDB; HIX0002290; -.
CC MIM; 123866; -.
CC GO; GO:0004129; F:cytochrome-c oxidase activity; TAS.
CC GO; GO:0007585; P:respiratory gaseous exchange; TAS.
CC InterPro; IPR002124; COX5B.
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CC ProDom; PD007270; COX5B; 1.
CC PROSITE; PS00848; COX5B; 1.
KW Direct protein sequencing; Inner membrane; Mitochondrion;
KW Oxidoreductase; Transit peptide; Zinc.
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FT CHAIN 32 129 Cytochrome c oxidase polypeptide Vb.
FT METAL 91 91 Zinc (potential).
FT METAL 113 113 Zinc (potential).
FT METAL 116 116 Zinc (potential).
FT CONFLICT 109 109 E -> Q (in Ref. 1).
SQ SEQUENCE 129 AA; 13696 MW; 877BF4CD334AC931 CRC64;

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Matches 11; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

QY 1 RGRPGAGAAARASGPGGGAP 19
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DB 20 RGPFGAAAMRSMASGGGVP 38

Search completed: September 11, 2005, 01:42:50
Job time : 28.4762 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 11, 2005, 01:30:14 ; Search time 7.33333 Seconds
(without alignments)
203.588 Million cell updates/sec

Title: US-09-529-206E-4_COPY_43_62

Perfect score: 107

Sequence: 1 RGRPGAGAAASGPGGAPR 20

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents AA:*
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5: /cgn2_6/ptodata/1/iaa/PCTUS COMB.pcp.*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pcp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	107	100.0	180	2	US-08-791-495-9
2	107	100.0	180	4	US-09-392-714-25
3	107	100.0	180	4	US-09-165-546D-15
4	107	100.0	180	4	US-09-341-829A-9
5	107	100.0	180	4	US-09-849-602-30
6	101	94.4	180	3	US-08-917-263B-8
7	101	94.4	180	4	US-09-751-798-8
8	99	92.5	180	2	US-08-791-495-7
9	99	92.5	180	4	US-09-341-829A-7
10	99	92.5	210	2	US-08-791-495-5
11	99	92.5	210	4	US-09-341-829A-5
12	63	58.9	860	4	US-09-352-991A-25681
13	60	56.1	160	4	US-09-352-991A-27091
14	60	56.1	366	4	US-09-902-540-13196
15	60	56.1	742	4	US-09-949-016-7729
16	60	56.1	928	1	US-08-442-248-2
17	60	56.1	928	1	US-08-440-815-2
18	60	56.1	928	3	US-08-486-449-2
19	60	56.1	928	4	US-08-578-684-2
20	60	56.1	1005	2	US-08-469-537A-103
21	59	55.1	210	4	US-09-252-991A-24923
22	59	55.1	330	1	US-08-118-270-21
23	59	55.1	330	5	PCT-US93-08528-21
24	59	55.1	877	2	US-08-673-789-2
25	58	54.2	282	4	US-09-949-016-8392
26	58	54.2	456	4	US-09-252-991A-17335
27	58	54.2	700	4	US-09-252-991A-28344

28	57	53.3	416	4	US-09-270-767-43018	Sequence 43018, A
29	57	53.3	857	4	US-09-902-540-12312	Sequence 12312, A
30	56	52.3	331	4	US-09-949-016-6708	Sequence 6708, Ap
31	56	52.3	421	4	US-09-252-991A-12326	Sequence 12326, A
32	56	52.3	432	4	US-09-252-991A-23622	Sequence 23622, A
33	55	51.4	191	4	US-09-252-991A-23951	Sequence 23951, A
34	55	51.4	289	4	US-09-252-991A-25496	Sequence 25496, A
35	55	51.4	289	4	US-09-949-016-8825	Sequence 8825, Ap
36	55	51.4	343	4	US-09-252-991A-23398	Sequence 23398, A
37	54.5	50.9	501	4	US-09-252-991A-32473	Sequence 32473, A
38	54.5	50.9	608	4	US-09-464-377-2	Sequence 2, Appli
39	54.5	50.9	608	4	US-09-464-377-3	Sequence 3, Appli
40	54	50.5	140	3	US-09-220-528-5	Sequence 5, Appli
41	54	50.5	140	4	US-09-347-613C-5	Sequence 5, Appli
42	54	50.5	140	4	US-09-347-613C-10	Sequence 10, Appli
43	54	50.5	140	4	US-09-662-183A-5	Sequence 5, Appli
44	54	50.5	140	4	US-09-662-183A-10	Sequence 10, Appli
45	54	50.5	159	3	US-09-220-528-12	Sequence 12, Appli

ALIGNMENTS

RESULT 1
US-08-791-495-9
; Sequence 9, Application US/08791495
; Patent No. 5811519
; GENERAL INFORMATION:
; APPLICANT: Leth, Bernard
; APPLICANT: Lucas, Sophie
; APPLICANT: De Smet, Charles
; APPLICANT: Godelaine, Daniele
; APPLICANT: Boon-Falleur, Thierry
; TITLE OF INVENTION: LL-1 TUMOR SPECIFIC GENES
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wolf, Greenfield & Sacks, P.C.
; STREET: 600 Atlantic Avenue
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/791,495
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Van Amsterdam, John R.
; REGISTRATION NUMBER: 40,212
; REFERENCE/DOCKET NUMBER: L0461/7005
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-720-3500
; TELEFAX: 617-720-2441
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 180 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-791-495-9

Query Match 100.0%; Score 107; DB 2; Length 180;

Best Local Similarity 100.0%; Pred. No. 2.9e-05;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGRPGAGAAASGPGGAPR 20

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DB 43 RGRPGAGAAASGPGGAPR 62

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;
; REFERENCE/DOCKET NUMBER: LUD 2166.4 CIP (09807811)
;
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 318-3000
; TELEFAX: (212) 318-3400
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 180 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 15
US-09-165-546D-15

Query Match 100.0%; Score 107; DB 4; Length 180;
Best Local Similarity 100.0%; Pred. No. 2.9e-05;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGRPGAGAAASGPGGGAPR 20
Db 43 RGRPGAGAAASGPGGGAPR 62

RESULT 4
US-09-341-829A-9
; Sequence 9, Application US/09341829A
; Patent No. 6794131
; GENERAL INFORMATION:
; APPLICANT: Leth, Bernard
; APPLICANT: Lucas, Sophie
; APPLICANT: De Smet, Charles
; APPLICANT: Godelaine, Daniele
; APPLICANT: Boon-Falleur, Thierry
; TITLE OF INVENTION: LAGE-1 TUMOR ASSOCIATED NUCLEIC ACIDS
; FILE REFERENCE: L0461/7066
; CURRENT APPLICATION NUMBER: US/09/341,829A
; CURRENT FILING DATE: 1999-10-18
; PRIOR APPLICATION NUMBER: US 08/791,495
; PRIOR APPLICATION NUMBER: PCT/US98/01445
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 9
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-341-829A-9

Query Match 100.0%; Score 107; DB 4; Length 180;
Best Local Similarity 100.0%; Pred. No. 2.9e-05;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGRPGAGAAASGPGGGAPR 20
Db 43 RGRPGAGAAASGPGGGAPR 62

RESULT 5
US-09-849-602-30
; Sequence 30, Application US/09849602
; Patent No. 6794501
; GENERAL INFORMATION:
; APPLICANT: Scanlan, Matthew J.
; APPLICANT: Old, Lloyd J.
; APPLICANT: Stockert, Elisabeth
; APPLICANT: Chen, Yao-Tseng
; TITLE OF INVENTION: Colon Cancer Antigen Panel
; FILE REFERENCE: L0461/7105(JRV)
; CURRENT APPLICATION NUMBER: US/09/849,602
; CURRENT FILING DATE: 2001-05-04
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 30
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Homo sapiens

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; REFERENCE/DOCKET NUMBER: LUD 2166.4 CIP (09807811)
;
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 318-3000
; TELEFAX: (212) 318-3400
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 180 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 15
US-09-165-546D-15

Query Match 100.0%; Score 107; DB 4; Length 180;
Best Local Similarity 100.0%; Pred. No. 2.9e-05;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGRPGAGAAASGPGGGAPR 20
Db 43 RGRPGAGAAASGPGGGAPR 62

RESULT 4
US-09-341-829A-9
; Sequence 9, Application US/09341829A
; Patent No. 6794131
; GENERAL INFORMATION:
; APPLICANT: Leth, Bernard
; APPLICANT: Lucas, Sophie
; APPLICANT: De Smet, Charles
; APPLICANT: Godelaine, Daniele
; APPLICANT: Boon-Falleur, Thierry
; TITLE OF INVENTION: LAGE-1 TUMOR ASSOCIATED NUCLEIC ACIDS
; FILE REFERENCE: L0461/7066
; CURRENT APPLICATION NUMBER: US/09/341,829A
; CURRENT FILING DATE: 1999-10-18
; PRIOR APPLICATION NUMBER: US 08/791,495
; PRIOR APPLICATION NUMBER: PCT/US98/01445
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 9
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-341-829A-9

Query Match 100.0%; Score 107; DB 4; Length 180;
Best Local Similarity 100.0%; Pred. No. 2.9e-05;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGRPGAGAAASGPGGGAPR 20
Db 43 RGRPGAGAAASGPGGGAPR 62

RESULT 5
US-09-849-602-30
; Sequence 30, Application US/09849602
; Patent No. 6794501
; GENERAL INFORMATION:
; APPLICANT: Scanlan, Matthew J.
; APPLICANT: Old, Lloyd J.
; APPLICANT: Stockert, Elisabeth
; APPLICANT: Chen, Yao-Tseng
; TITLE OF INVENTION: Colon Cancer Antigen Panel
; FILE REFERENCE: L0461/7105(JRV)
; CURRENT APPLICATION NUMBER: US/09/849,602
; CURRENT FILING DATE: 2001-05-04
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 30
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Homo sapiens

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; APPLICATION NUMBER: US/08/791,495
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Van Amsterdam, John R.
; REGISTRATION NUMBER: 40,212
; REFERENCE/DOCKET NUMBER: L0461/7005
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-720-3500
; TELEFAX: 617-720-2441
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 180 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-791-495-7

Query Match          92.5%; Score 99; DB 2; Length 180;
Best Local Similarity 95.0%; Pred. No. 0.00023;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RGPARGAARASGPGGAPR 20
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Db 43 RGPARGAARASGPRGGAPR 62

RESULT 9
US-09-341-829A-7
; Sequence 7, Application US/09341829A
; Patent No. 6794131
; GENERAL INFORMATION:
; APPLICANT: Leth,, Bernard
; APPLICANT: Lucas, Sophie
; APPLICANT: De Smet, Charles
; APPLICANT: Godelaine, Daniele
; APPLICANT: Boon-Falleur, Thierry
; TITLE OF INVENTION: LAGE-1 TUMOR ASSOCIATED NUCLEIC ACIDS
; FILE REFERENCE: L0461/7066
; CURRENT APPLICATION NUMBER: US/09/341,829A
; PRIOR FILING DATE: 1999-10-18
; PRIOR APPLICATION NUMBER: US 08/791,495
; PRIOR APPLICATION NUMBER: PCT/US98/01445
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-341-829A-7

Query Match          92.5%; Score 99; DB 4; Length 180;
Best Local Similarity 95.0%; Pred. No. 0.00023;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RGPARGAARASGPGGAPR 20
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Db 43 RGPARGAARASGPRGGAPR 62

RESULT 10
US-08-791-495-5
; Sequence 5, Application US/08791495
; Patent No. 5811519
; GENERAL INFORMATION:
; APPLICANT: Leth,, Bernard
; APPLICANT: Lucas, Sophie
; APPLICANT: De Smet, Charles
; APPLICANT: Godelaine, Daniele
; APPLICANT: Boon-Falleur, Thierry
; TITLE OF INVENTION: LL-1 TUMOR SPECIFIC GENES
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
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; ADDRESSEE: Wolf, Greenfield & Sacker, P.C.
; STREET: 600 Atlantic Avenue
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APLICATION NUMBER: US/08/791,495
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Van Amsterdam, John R.
; REGISTRATION NUMBER: 40,212
; REFERENCE/DOCKET NUMBER: L0461/7005
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-720-3500
; TELEFAX: 617-720-2441
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 210 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-791-495-5

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Best Local Similarity 95.0%; Pred. No. 0.00027;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RGPARGAARASGPGGGAPR 20
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Db 43 RGPARGAARASGPRGGAPR 62

RESULT 11
US-09-341-829A-5
; Sequence 5, Application US/09341829A
; Patent No. 6794131
; GENERAL INFORMATION:
; APPLICANT: Leth,, Bernard
; APPLICANT: Lucas, Sophie
; APPLICANT: De Smet, Charles
; APPLICANT: Godelaine, Daniele
; APPLICANT: Boon-Falleur, Thierry
; TITLE OF INVENTION: LAGE-1 TUMOR ASSOCIATED NUCLEIC ACIDS
; FILE REFERENCE: L0461/7066
; CURRENT APPLICATION NUMBER: US/09/341,829A
; PRIOR FILING DATE: 1999-10-18
; PRIOR APPLICATION NUMBER: US 08/791,495
; PRIOR APPLICATION NUMBER: PCT/US98/01445
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 210
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-341-829A-5

Query Match          92.5%; Score 99; DB 4; Length 210;
Best Local Similarity 95.0%; Pred. No. 0.00027;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RGPARGAARASGPGGGAPR 20
   |||||
Db 43 RGPARGAARASGPRGGAPR 62

RESULT 12
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US-09-252-991A-25681
; Sequence 25681, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 25681
; LENGTH: 860
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-25681

Query Match      58.9%; Score 63; DB 4; Length 860;
Best Local Similarity 63.2%; Pred. No. 11;
Matches 12; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 RGRGAGAAASGPGGGAP 19
| | | | | : | | | |
Db 738 RKRGRSTAARQTGSGGGTP 756

RESULT 13
US-09-252-991A-27091
; Sequence 27091, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 27091
; LENGTH: 160
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-27091

Query Match      56.1%; Score 60; DB 4; Length 160;
Best Local Similarity 63.6%; Pred. No. 5.3;
Matches 14; Conservative 0; Mismatches 4; Indels 4; Gaps 1;

QY 3 PRGAGAAASG----PGGGAP 20
| | | | | | | | | |
Db 103 PRGAGAAASGRCRRPAGRP 124

RESULT 14
US-09-902-540-13196
; Sequence 13196, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
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US-09-902-540-13196
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 13196
; LENGTH: 366
; TYPE: PRT
; ORGANISM: Myxococcus xanthus
US-09-902-540-13196

Query Match      56.1%; Score 60; DB 4; Length 366;
Best Local Similarity 66.7%; Pred. No. 11;
Matches 12; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 3 PRGAGAAASGPGGGAP 20
| | | | | : | | | |
Db 69 PRPAGTAPAGPGATAP 86

RESULT 15
US-09-949-016-7729
; Sequence 7729, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7729
; LENGTH: 742
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-7729

Query Match      56.1%; Score 60; DB 4; Length 742;
Best Local Similarity 61.1%; Pred. No. 22;
Matches 11; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 2 GPRGAGAAASGPGGGAP 19
| | | | | | | | | |
Db 64 GPPGAGDRGGGPGGGGP 81

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OM protein - protein search, using sw model

Run on: September 11, 2005, 01:43:05 ; Search time 27.0476 Seconds
(without alignments)
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Title: US-09-529-206E-4_COPY_43_62

Perfect score: 107

Sequence: 1 RGRGAGAAASGPGGAPR 20

Scoring table: BLOSUM62

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Searched: 1777461 seqs, 39431504 residues

Total number of hits satisfying chosen parameters: 1777461

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*
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5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
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11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
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16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep.*
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18: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
19: /cgn2_6/ptodata/1/pubpaa/US11A_PUBCOMB.pep.*
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21: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	107	100.0	179	17	US-10-482-029-202
2	107	100.0	180	10	US-09-849-602-30
3	107	100.0	180	14	US-10-207-655-71
4	107	100.0	180	15	US-10-026-066-3
5	107	100.0	180	15	US-10-117-937-74
6	107	100.0	180	15	US-10-295-027-386
7	107	100.0	180	15	US-10-296-734-832
8	107	100.0	180	15	US-10-188-832-139
9	107	100.0	180	16	US-10-777-053-11
10	107	100.0	180	16	US-10-751-088-15
11	107	100.0	180	16	US-10-657-022-74
12	107	100.0	179	17	US-10-482-029-202
13	107	100.0	180	10	US-09-849-602-30
14	107	100.0	180	14	US-10-207-655-71
15	107	100.0	180	15	US-10-026-066-3
16	107	100.0	180	15	US-10-117-937-74
17	107	100.0	180	15	US-10-295-027-386
18	107	100.0	180	15	US-10-296-734-832
19	107	100.0	180	15	US-10-188-832-139
20	107	100.0	180	16	US-10-777-053-11
21	107	100.0	180	16	US-10-751-088-15
22	107	100.0	180	16	US-10-657-022-74

12	107	100.0	180	16	US-10-837-217-11	Sequence 11, Appl
13	107	100.0	180	16	US-10-877-373-9	Sequence 9, Appl
14	107	100.0	180	16	US-10-723-860-1270	Sequence 1270, Ap
15	107	100.0	180	17	US-10-871-708-7	Sequence 7, Appl
16	107	100.0	180	18	US-10-895-523-3	Sequence 3, Appl
17	107	100.0	180	18	US-10-182-506A-3	Sequence 3, Appl
18	107	100.0	180	18	US-10-756-149-5024	Sequence 5024, Ap
19	107	100.0	180	20	US-11-067-064-74	Sequence 74, Appl
20	107	100.0	337	9	US-09-821-883-27	Sequence 27, Appl
21	102	95.3	30	15	US-10-296-734-1404	Sequence 1404, Ap
22	102	95.3	3541	15	US-10-296-734-1454	Sequence 1454, Ap
23	101	94.4	180	9	US-09-751-798-8	Sequence 8, Appl
24	101	94.4	180	13	US-10-023-182-8	Sequence 8, Appl
25	101	94.4	180	14	US-10-364-614-14	Sequence 14, Appl
26	99	92.5	135	15	US-10-295-027-388	Sequence 388, App
27	99	92.5	135	15	US-10-188-832-141	Sequence 141, App
28	99	92.5	180	14	US-10-146-473-69	Sequence 69, Appl
29	99	92.5	180	15	US-10-117-937-75	Sequence 75, Appl
30	99	92.5	180	15	US-10-296-734-834	Sequence 834, App
31	99	92.5	180	16	US-10-468-406-4	Sequence 4, Appl
32	99	92.5	180	16	US-10-657-022-75	Sequence 75, Appl
33	99	92.5	180	16	US-10-877-373-7	Sequence 7, Appl
34	99	92.5	180	20	US-11-067-064-75	Sequence 75, Appl
35	99	92.5	210	14	US-10-157-031-88	Sequence 88, Appl
36	99	92.5	210	15	US-10-117-937-76	Sequence 76, Appl
37	99	92.5	210	16	US-10-657-022-76	Sequence 76, Appl
38	99	92.5	210	16	US-10-877-373-5	Sequence 5, Appl
39	99	92.5	210	20	US-11-067-064-76	Sequence 76, Appl
40	95	88.8	20	15	US-10-313-986-496	Sequence 496, App
41	95	88.8	20	16	US-10-775-972-496	Sequence 496, App
42	95	88.8	20	18	US-10-922-124-496	Sequence 496, App
43	94	87.9	30	15	US-10-296-734-1436	Sequence 1436, Ap
44	85	79.4	30	15	US-10-296-734-1402	Sequence 1402, Ap
45	77	72.0	30	15	US-10-296-734-1434	Sequence 1434, Ap

ALIGNMENTS

RESULT 1

US-10-482-029-202
; Sequence 202, Application US/10482029
; Publication No. US20050037445A1
; GENERAL INFORMATION:
; APPLICANT: ODIN medical A/S
; TITLE OF INVENTION: Oncology drug innovation
; FILE REFERENCE: P 573 PC00
; CURRENT APPLICATION NUMBER: US/10/482,029
; CURRENT FILING DATE: 2003-12-29
; NUMBER OF SEQ ID NOS: 437
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 202
; LENGTH: 179
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-482-029-202

Query Match 100.0%; Score 107; DB 17; Length 179;
Best Local Similarity 100.0%; Pred. No. 0.00057;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGRGAGAAASGPGGAPR 20

DB 43 RGRGAGAAASGPGGAPR 62

RESULT 2

US-09-849-602-30
; Sequence 30, Application US/09849602
; Publication No. US20030165834A1
; GENERAL INFORMATION:
; APPLICANT: Scanlan, Matthew J.
; APPLICANT: Old, Lloyd J.

```
; APPLICANT: Stockert, Elisabeth
; APPLICANT: Chen, Yao-Tseeng
; TITLE OF INVENTION: Colon Cancer Antigen Panel
; FILE REFERENCE: L0461/7105(JRV)
; CURRENT APPLICATION NUMBER: US/09/849,602
; CURRENT FILING DATE: 2001-05-04
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 30
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-849-602-30

Query Match      100.0%; Score 107; DB 10; Length 180;
Best Local Similarity 100.0%; Pred. No. 0.00058;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 RGRGAGAAARASGPGGGAPR 20
Db      43 RGRGAGAAARASGPGGGAPR 62

RESULT 3
US-10-207-655-71
; Sequence 71, Application US/10207655
; Publication No. US20030118592A1
; GENERAL INFORMATION:
; APPLICANT: Ledbetter, Jeffrey A.
; APPLICANT: Hayden-Ledbetter, Martha S.
; TITLE OF INVENTION: BINDING DOMAIN-IMMUNOGLOBULIN FUSION PROTEINS
; FILE REFERENCE: 390069.401C1
; CURRENT APPLICATION NUMBER: US/10/207,655
; CURRENT FILING DATE: 2002-07-25
; NUMBER OF SEQ ID NOS: 426
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 71
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-207-655-71

Query Match      100.0%; Score 107; DB 14; Length 180;
Best Local Similarity 100.0%; Pred. No. 0.00058;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 RGRGAGAAARASGPGGGAPR 20
Db      43 RGRGAGAAARASGPGGGAPR 62

RESULT 4
US-10-026-066-3
; Sequence 3, Application US/10026066
; Publication No. US20030215425A1
; GENERAL INFORMATION:
; APPLICANT: Simard, John J. L.
; APPLICANT: Diamond, David C.
; TITLE OF INVENTION: EPIPOPE SYNCHRONIZATION IN ANTIGEN
; TITLE OF INVENTION: PRESENTING CELLS
; FILE REFERENCE: CTLIMM.21CPIC
; CURRENT APPLICATION NUMBER: US/10/026,066
; CURRENT FILING DATE: 2001-12-07
; PRIOR APPLICATION NUMBER: 09/561,074
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 09/560,465
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 09/561,572
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 09/561,571
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: PCT/US01/13806
; PRIOR FILING DATE: 2001-04-27

; APPLICANT: Stockert, Elisabeth
; APPLICANT: Chen, Yao-Tseeng
; TITLE OF INVENTION: Colon Cancer Antigen Panel
; FILE REFERENCE: L0461/7105(JRV)
; CURRENT APPLICATION NUMBER: US/09/849,602
; CURRENT FILING DATE: 2001-05-04
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 30
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-849-602-30

Query Match      100.0%; Score 107; DB 10; Length 180;
Best Local Similarity 100.0%; Pred. No. 0.00058;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 RGRGAGAAARASGPGGGAPR 20
Db      43 RGRGAGAAARASGPGGGAPR 62

RESULT 5
US-10-117-937-74
; Sequence 74, Application US/10117937
; Publication No. US20030220239A1
; GENERAL INFORMATION:
; APPLICANT: CTL IMMUNO THERAPIES CORP.
; APPLICANT: SIMARD, John, J.L.
; APPLICANT: DIAMOND, David, C.
; APPLICANT: LIU, Liping
; APPLICANT: XIE, Zhidong
; TITLE OF INVENTION: EPIPOPE SEQUENCES
; FILE REFERENCE: CTLIMM.027A
; CURRENT APPLICATION NUMBER: US/10/117,937
; CURRENT FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: US 60/282,211
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 60/337,017
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: US 60/363,210
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 602
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 74
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-117-937-74

Query Match      100.0%; Score 107; DB 15; Length 180;
Best Local Similarity 100.0%; Pred. No. 0.00058;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 RGRGAGAAARASGPGGGAPR 20
Db      43 RGRGAGAAARASGPGGGAPR 62

RESULT 6
US-10-295-027-386
; Sequence 386, Application US/10295027
; Publication No. US20030232350A1
; GENERAL INFORMATION:
; APPLICANT: Afar, Daniel
; APPLICANT: Aziz, Natasha
; APPLICANT: Ginsberg, Wendy M.
; APPLICANT: Gish, Kurt C.
; APPLICANT: Glynn, Richard
; APPLICANT: Hevezi, Peter A.
; APPLICANT: Mack, David H.
; APPLICANT: Murray, Richard
; APPLICANT: Watson, Susan R.
; APPLICANT: Eos Biotechnology, Inc.
; TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and
; TITLE OF INVENTION: Methods of Screening for Modulators of Cancer
; FILE REFERENCE: 018501-012500US
; CURRENT APPLICATION NUMBER: US/10/295,027
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; CURRENT FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: US 09/663,733
; PRIOR FILING DATE: 2000-09-15
; PRIOR APPLICATION NUMBER: US 60/350,666
; PRIOR FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 60/335,394
; PRIOR FILING DATE: 2001-11-15
; PRIOR APPLICATION NUMBER: US 60/332,464
; PRIOR FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: US 60/334,393
; PRIOR FILING DATE: 2001-11-29
; PRIOR APPLICATION NUMBER: US 60/340,376
; PRIOR FILING DATE: 2001-12-14
; PRIOR APPLICATION NUMBER: US 60/347,211
; PRIOR FILING DATE: 2002-01-08
; PRIOR APPLICATION NUMBER: US 60/347,349
; PRIOR FILING DATE: 2002-01-10
; PRIOR APPLICATION NUMBER: US 60/355,250
; PRIOR FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: US 60/356,714
; PRIOR FILING DATE: 2002-02-13
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1386
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 386
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-295-027-386
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Query Match 100.0%; Score 107; DB 15; Length 180;
Best Local Similarity 100.0%; Pred. No. 0.00058;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 RGRGAGAAASGPGGAPR 20
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DB 43 RGRGAGAAASGPGGAPR 62
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RESULT 7

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US-10-296-734-832
; Sequence 832, Application US/10296734
; Publication No. US20040054137A1
; GENERAL INFORMATION:
; APPLICANT: Thompson, Scott A
; APPLICANT: Ramshaw, Ian A
; TITLE OF INVENTION: Synthetic molecules and uses therefor
; FILE REFERENCE: Savine
; CURRENT APPLICATION NUMBER: US/10/296,734
; CURRENT FILING DATE: 2003-08-04
; PRIOR APPLICATION NUMBER: AU PQ7761/00
; PRIOR FILING DATE: 2000-05-26
; NUMBER OF SEQ ID NOS: 1507
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 832
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: NYSOLA consensus polypeptide
US-10-296-734-832
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Query Match 100.0%; Score 107; DB 15; Length 180;
Best Local Similarity 100.0%; Pred. No. 0.00058;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 RGRGAGAAASGPGGAPR 20
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DB 43 RGRGAGAAASGPGGAPR 62
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RESULT 8

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US-10-188-832-139
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; Sequence 139, Application US/10188832
; Publication No. US20040076955A1
; GENERAL INFORMATION:
; APPLICANT: Mack, David H.
; APPLICANT: Azi, Natasha
; APPLICANT: Eos Biotechnology, Inc.
; TITLE OF INVENTION: Methods of Diagnosis of Bladder Cancer, Compositions
; TITLE OF INVENTION: and Methods of Screening for Modulators of Bladder
; TITLE OF INVENTION: Cancer
; FILE REFERENCE: 018501-002330US
; CURRENT APPLICATION NUMBER: US/10/188,832
; CURRENT FILING DATE: 2002-11-22
; PRIOR APPLICATION NUMBER: US 60/302,814
; PRIOR FILING DATE: 2001-07-03
; PRIOR APPLICATION NUMBER: US 60/310,099
; PRIOR FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: US 60/343,705
; PRIOR FILING DATE: 2001-11-08
; PRIOR APPLICATION NUMBER: US 60/350,666
; PRIOR FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 60/372,246
; PRIOR FILING DATE: 2002-04-12
; NUMBER OF SEQ ID NOS: 207
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 139
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-188-832-139
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Query Match 100.0%; Score 107; DB 15; Length 180;
Best Local Similarity 100.0%; Pred. No. 0.00058;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 RGRGAGAAASGPGGAPR 20
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DB 43 RGRGAGAAASGPGGAPR 62
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RESULT 9

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US-10-777-053-11
; Sequence 11, Application US/10777053
; Publication No. US20040132088A1
; GENERAL INFORMATION:
; APPLICANT: Simard, John J. L.
; APPLICANT: Diamond, David C.
; APPLICANT: Qiu, Zhiyong
; APPLICANT: Lei, Xiang-Dong
; TITLE OF INVENTION: EXPRESSION VECTORS ENCODING EPITOPES OF
; TITLE OF INVENTION: TARGET-ASSOCIATED ANTIGENS AND METHODS FOR THEIR DESIGN
; FILE REFERENCE: MAN/K.022C1
; CURRENT APPLICATION NUMBER: US/10/777,053
; CURRENT FILING DATE: 2004-02-10
; PRIOR APPLICATION NUMBER: 10/292,413
; PRIOR FILING DATE: 2002-11-07
; PRIOR APPLICATION NUMBER: 60/336,968
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 979
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-777-053-11
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Query Match 100.0%; Score 107; DB 16; Length 180;
Best Local Similarity 100.0%; Pred. No. 0.00058;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 RGRGAGAAASGPGGAPR 20
   |||||
DB 43 RGRGAGAAASGPGGAPR 62
```

```
RESULT 10
US-10-751-088-15
; Sequence 15, Application US/10751088
; Publication No. US20040158044A1
; GENERAL INFORMATION:
; APPLICANT: Knuth, Alexander; Jager, Elke; Chen, Yao, Scanlan, Matt;
; Gure, Ali, Old, Lloyd, Ritter, Gerd
; TITLE OF INVENTION: ISOLATED PEPTIDES CORRESPONDING TO AMINO ACID
; SEQUENCES OF NY-ESO-1, WHICH BIND TO MHC CLASS I AND MHC CH
; USES THEREOF
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FULBRIGHT & JAWORSKI LLP
; STREET: 666 Fifth Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10158
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Word
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10751,088
; FILING DATE: 02-Jan-2004
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/165,546D
; FILING DATE: 02-Oct-1998
; APPLICATION NUMBER: 09/062,422
; FILING DATE: April 17, 1998
; APPLICATION NUMBER: 08/937,263
; FILING DATE: September 15, 1997
; APPLICATION NUMBER: US 08/725,182
; FILING DATE: October 3, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, Norman D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: LUD 2166.4 CIP (09807811)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 318-3000
; TELEFAX: (212) 318-3400
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 180 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 15
US-10-751-088-15
Query Match 100.0%; Score 107; DB 16; Length 180;
Best Local Similarity 100.0%; Pred. No. 0.00058;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RGPRGAGAAASGPGGGAPR 20
Db 43 RGPRGAGAAASGPGGGAPR 62

RESULT 11
US-10-657-022-74
; Sequence 74, Application US/10657022
; Publication No. US20040180354A1
; GENERAL INFORMATION:
; APPLICANT: Simard, John J. L.
; APPLICANT: Diamond, David C.
; APPLICANT: Liu, Liping
; APPLICANT: Liu, Zheng
; TITLE OF INVENTION: EPITOPE SEQUENCES
; FILE REFERENCE: MANK.032A
; CURRENT APPLICATION NUMBER: US/10/657,022
```

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; CURRENT FILING DATE: 2003-09-04
; PRIOR APPLICATION NUMBER: 60/409123
; PRIOR FILING DATE: 2002-09-06
; NUMBER OF SEQ ID NOS: 610
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 74
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-657-022-74
Query Match 100.0%; Score 107; DB 16; Length 180;
Best Local Similarity 100.0%; Pred. No. 0.00058;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RGPRGAGAAASGPGGGAPR 20
Db 43 RGPRGAGAAASGPGGGAPR 62

RESULT 12
US-10-837-217-11
; Sequence 11, Application US/10837217
; Publication No. US20040203051A1
; GENERAL INFORMATION:
; APPLICANT: Simard, John J. L.
; APPLICANT: Diamond, David C.
; APPLICANT: Qiu, Zhiyong
; APPLICANT: Lei, Xiang-Dong
; TITLE OF INVENTION: EXPRESSION VECTORS ENCODING EPITOPES OF
; TARGET-ASSOCIATED ANTIGENS AND METHODS FOR THEIR DESIGN
; FILE REFERENCE: MANK.022C2
; CURRENT APPLICATION NUMBER: US/10/837,217
; CURRENT FILING DATE: 2004-04-30
; PRIOR APPLICATION NUMBER: 10/292,413
; PRIOR FILING DATE: 2002-11-07
; PRIOR APPLICATION NUMBER: 60/336,968
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 979
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-837-217-11
Query Match 100.0%; Score 107; DB 16; Length 180;
Best Local Similarity 100.0%; Pred. No. 0.00058;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RGPRGAGAAASGPGGGAPR 20
Db 43 RGPRGAGAAASGPGGGAPR 62

RESULT 13
US-10-877-373-9
; Sequence 9, Application US/10877373
; Publication No. US20040234541A1
; GENERAL INFORMATION:
; APPLICANT: Leth, Bernard
; APPLICANT: Lucas, Sophie
; APPLICANT: De Smet, Charles
; APPLICANT: Godelaine, Daniele
; APPLICANT: Boon-Falleur, Thierry
; TITLE OF INVENTION: LAGE-1 TUMOR ASSOCIATED NUCLEIC ACIDS
; FILE REFERENCE: L0461/7066
; CURRENT APPLICATION NUMBER: US/10/877,373
; CURRENT FILING DATE: 2004-06-25
; PRIOR APPLICATION NUMBER: US/09/341,829
; PRIOR FILING DATE: 1999-10-18
; PRIOR APPLICATION NUMBER: US 08/791,495
; PRIOR APPLICATION NUMBER: PCT/US98/01445
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; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 9
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-877-373-9

Query Match 100.0%; Score 107; DB 16; Length 180;
Best Local Similarity 100.0%; Pred. No. 0.00058;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGRGAGAAARASGPGGAPR 20
Db 43 RGRGAGAAARASGPGGAPR 62

RESULT 14

US-10-723-860-1270
; Sequence 1270, Application US/10723860
; Publication No. US20040253606A1
; GENERAL INFORMATION:
; APPLICANT: Aziz, Natasha
; APPLICANT: Ginsburg, Wendy M.
; APPLICANT: Zlotnik, Albert
; TITLE OF INVENTION: Methods of Diagnosis of Soft Tissue Sarcoma, Compositions &
; TITLE OF INVENTION: Methods for Screening for Soft Tissue Sarcoma Modulators
; FILE REFERENCE: 05882.0193.NPUS01
; CURRENT APPLICATION NUMBER: US/10/723,860
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: 60/429,739
; PRIOR FILING DATE: 2002-11-26
; NUMBER OF SEQ ID NOS: 8393
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1270
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-723-860-1270

Query Match 100.0%; Score 107; DB 16; Length 180;
Best Local Similarity 100.0%; Pred. No. 0.00058;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGRGAGAAARASGPGGAPR 20
Db 43 RGRGAGAAARASGPGGAPR 62

RESULT 15

US-10-871-708-7
; Sequence 7, Application US/10871708
; Publication No. US20050118186A1
; GENERAL INFORMATION:
; APPLICANT: Chiang, Chih-Sheng
; TITLE OF INVENTION: COMBINATIONS OF TUMOR-ASSOCIATED
; TITLE OF INVENTION: ANTIGENS IN COMPOSITIONS FOR VARIOUS TYPES OF CANCERS
; FILE REFERENCE: MANNK.035A
; CURRENT APPLICATION NUMBER: US/10/871,708
; CURRENT FILING DATE: 2004-06-17
; PRIOR APPLICATION NUMBER: 60/479,554
; PRIOR FILING DATE: 2003-06-17
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Autoimmunogenic Cancer
US-10-871-708-7

Query Match 100.0%; Score 107; DB 17; Length 180;
Best Local Similarity 100.0%; Pred. No. 0.00058;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGRGAGAAARASGPGGAPR 20
Db 43 RGRGAGAAARASGPGGAPR 62

Search completed: September 11, 2005, 02:07:10
Job time : 27.0476 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 11, 2005, 01:19:58 ; Search time 14.3333 Seconds
(without alignments)
269.833 Million cell updates/sec

Title: US-09-529-206E-4_COPY_127_136

Perfect score: 47
Sequence: 1 TVSGNLTIR 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:.*
1: Geneseq1980s:.*
2: Geneseq1990s:.*
3: Geneseq2000s:.*
4: Geneseq2001s:.*
5: Geneseq2002s:.*
6: Geneseq2003as:.*
7: Geneseq2003bs:.*
8: Geneseq2004s:.*

pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	47	100.0	10	2	Aay05980 Human can
2	47	100.0	10	2	Aay05988 Human can
3	47	100.0	14	4	Aae07788 Human NY
4	47	100.0	14	4	Aae07728 Human NY
5	47	100.0	15	4	Aae07726 Human NY
6	47	100.0	15	4	Aae07727 Human NY
7	47	100.0	15	4	Aae07786 Human NY
8	47	100.0	15	4	Aae07787 Human NY
9	47	100.0	18	3	Aay52440 Human tum
10	47	100.0	18	4	Aab69940 Human NY-
11	47	100.0	18	4	Aab69944 Human NY-
12	47	100.0	18	4	AAU01544 HLA-DR53
13	47	100.0	18	4	AAU01540 HLA-DR53
14	47	100.0	18	4	Aae07769 Human NY
15	47	100.0	20	4	Aae07742 Human ESO
16	47	100.0	20	8	ADI19891 Human HLA
17	47	100.0	20	8	ADI19048 Human HLA
18	47	100.0	20	8	ADJ58397 Peptide p
19	47	100.0	25	4	Aae07718 Human NY
20	47	100.0	25	7	ADD71521 HLA-DP4 b
21	47	100.0	27	4	Aae07717 Human NY
22	47	100.0	30	5	AAU85110 Human NYN
23	47	100.0	36	5	ABG79131 Human NY-
24	47	100.0	54	8	ADG89697 Class II
25	47	100.0	123	8	ADQ10452 Epitope 1

26	47	100.0	179	8	ADK68648	Adk68648 Epitope 1
27	47	100.0	179	8	ADK68657	Adk68657 Epitope 1
28	47	100.0	179	8	ADQ10455	Adq10455 Epitope 1
29	47	100.0	180	2	AAW62584	Aaw62584 Cancer as
30	47	100.0	180	2	AAW69655	Aaw69655 Human NY-
31	47	100.0	180	2	AAU05965	AAu05965 Human can
32	47	100.0	180	3	AAU52430	AAu52430 Human tum
33	47	100.0	180	3	AAU70862	AAu70862 Human tum
34	47	100.0	180	3	AAU03154	AAu03154 Human oes
35	47	100.0	180	4	AAU69946	AAu69946 Human NY-
36	47	100.0	180	4	AAU67164	AAu67164 Amino aci
37	47	100.0	180	4	AAU01535	AAu01535 Human NY-
38	47	100.0	180	4	AAE07714	AAe07714 Human NY
39	47	100.0	180	5	AAU84818	AAu84818 Human NYN
40	47	100.0	180	5	AAU11543	AAu11543 Human tum
41	47	100.0	180	6	ABR58672	ABr58672 Human can
42	47	100.0	180	6	ABR48210	ABr48210 Human bla
43	47	100.0	180	6	ABU56508	ABu56508 Lung canc
44	47	100.0	180	6	ABU56694	ABu56694 Lung canc
45	47	100.0	180	6	ABP74198	ABp74198 Human NY-

ALIGNMENTS

RESULT 1
AAY05980
ID AAY05980 standard; peptide; 10 AA.
XX AC AAY05980;
XX
DT 16-AUG-1999 (first entry)
XX
DE Human cancer antigen NY ESO-1/CAG-3 ORF1 cancer peptide ESO10-127.
XX NY ESO-1/CAG-3 gene; CAG-3 gene; cancer peptide; antigen; human;
KW leukaemia; non-Hodgkins lymphoma; Hodgkins lymphoma; lung cancer;
KW metastasis; melanoma; adenocarcinoma; thymoma; colon cancer;
KW uterine cancer; breast cancer; prostate cancer; ovarian cancer;
KW cervical cancer; bladder cancer; kidney cancer; pancreatic cancer;
KW liver cancer; sarcoma; tumour; diagnosis; immunotherapy; therapy;
KW vaccine.
XX OS Homo sapiens.
XX
XX
PN WO9918206-A2.
XX
XX
PD 15-APR-1999.
XX
XX
PF 21-SEP-1998; 98WO-US019609.
XX
XX
PR 08-OCT-1997; 97US-0061428P.
XX
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
XX
PI Wang RF, Rosenberg SA;
XX
XX
DR WPI; 1999-277270/23.
XX
XX
PT Cancer antigen NY ESO1/CAG-3.
XX
XX
PS Claim 17; Page 64; 88pp; English.
XX
XX
CC This sequence represents cancer peptide ESO10-127 that corresponds to
CC amino acid residues 127-136 of human ESO-1/CAG-3 (or CAG-3) ORF1 (see
CC AAY05985), a new and potent tumour antigen capable of eliciting an
CC antigen specific immune response by T cells. Cancer peptides derived from
CC CAG-3 ORF1, CAG-3 ORF2 (see AAY05966), portions of them and their
CC variants (see AAY05967-87), are useful as cancer vaccines that protect
CC against cancer. The invention provides: vectors and host cells (also
CC useful as vaccines); a method of diagnosis of cancer or precancer; a
CC transgenic animal; antisense oligonucleotides that inhibit expression of
CC the cancer peptide or tumour antigen; antibodies reacting with a CAG-3

CC cancer peptide, useful in diagnostic and detection assays; and methods
 CC for preventing or inhibiting cancer by administering a cancer peptide,
 CC with or without an HLA molecule. The cancer peptides form part of, or are
 CC derived from, cancers such as primary or metastatic melanoma, thymoma,
 CC lymphoma, sarcoma, lung cancer, liver cancer, leukaemia, uterine cancer,
 CC cervical cancer, bladder cancer, kidney cancer and adenocarcinomas such
 CC as breast, prostate, ovarian, pancreatic and thyroid cancers. Melanoma is
 CC treated by inducing cancer-specific T cells in vitro for subsequent
 CC return to a patient
 XX
 SQ Sequence 10 AA;

Query Match 100.0%; Score 47; DB 2; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.0035;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TVSGNLTIR 10
 |||||
 DB 1 TVSGNLTIR 10

RESULT 2
 AAY05988
 ID AAY05988 standard; peptide; 10 AA.

AC AAY05988;

XX 16-AUG-1999 (first entry)

XX Human cancer antigen NY ESO-1/CAG-3 HLA peptide motif.

XX NY ESO-1/CAG-3 gene; CAG-3 gene; cancer peptide; antigen; human;
 KW leukaemia; non-Hodgkins lymphoma; Hodgkins lymphoma; lung cancer;
 KW metastasis; melanoma; adenocarcinoma; thymoma; colon cancer;
 KW uterine cancer; breast cancer; prostate cancer; ovarian cancer;
 KW cervical cancer; bladder cancer; kidney cancer; pancreatic cancer;
 KW liver cancer; sarcoma; tumour; diagnosis; kidney cancer; immunotherapy;
 KW vaccine; human leukocyte antigen; HLA.

XX Homo sapiens.

XX WO9918206-A2.

XX 15-APR-1999.

XX 21-SEP-1998; 98WO-US019609.

XX 08-OCT-1997; 97US-0061428P.

XX (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX Wang RF, Rosenberg SA;

XX WPI; 1999-277270/23.

XX Cancer antigen NY ESO1/CAG-3.

XX Example 10; Page 42; 88pp; English.

XX This peptide was identified as an HLA peptide motif following a screen
 CC for epitopes from the coding region of human NY ESO-1/CAG-3 ORF1 (see
 CC AX58599). 30 Epitopes (see AAY05988-Y06017) were identified. The present
 CC peptide (ranked 1) corresponds to amino acid residues 127-136 of CAG-1
 CC ORF1 (see AAY05965). CAG-1 is a new and potent tumour antigen capable of
 CC eliciting an antigen specific immune response by T cells. Cancer peptides
 CC (see AAY05967-87) derived from CAG-3, portions of CAG-3 and their
 CC variants, are useful as cancer vaccines. A claimed method of preventing
 CC or inhibiting cancer involves administering a cancer peptide, with or
 CC without an HLA molecule. The cancer peptides form part of, or are derived
 CC from, cancers such as primary or metastatic melanoma, thymoma, lymphoma,
 CC sarcoma, lung cancer, liver cancer, leukaemia, uterine cancer, cervical
 CC cancer, bladder cancer, kidney cancer and adenocarcinomas such as breast,
 CC prostate, ovarian, pancreatic and thyroid cancers

XX Sequence 10 AA;

Query Match 100.0%; Score 47; DB 2; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.0035;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TVSGNLTIR 10
 |||||
 DB 1 TVSGNLTIR 10

RESULT 3
 AAE07788
 ID AAE07788 standard; peptide; 14 AA.

XX AAE07788;

XX 06-NOV-2001 (first entry)

XX Human NY ESO-1 peptide #22 to characterise epitope recognised by TE4-1.

XX Human; major histocompatibility complex; MHC; vaccine; metastasis;
 KW class II restricted T cell epitope; MHC-II epitope; cancer antigen;
 KW NY ESO-1 protein; CD4+ T lymphocyte; human leukocyte antigen; HLA;
 KW tumour-specific humoral-mediated immunity; cancer; cytostatic;
 KW immunotherapy.

XX Homo sapiens.

XX WO200155393-A2.

XX 02-AUG-2001.

XX 26-JAN-2001; 2001WO-US002765.

XX 28-JAN-2000; 2000US-0179004P.

XX 29-SEP-2000; 2000US-0237107P.

XX (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX Wang R, Rosenberg SA, Zeng G;

XX WPI; 2001-496851/54.

XX New NY-ESO cancer peptide or MHC class II restricted T cell epitopes,
 PT useful as immunogen and vaccine for inhibiting cancer in a mammal or as
 PT protection from metastasis.

XX Example 6; Fig 6A; 134pp; English.

XX The invention relates to the identification and isolation of major
 CC histocompatibility (MHC) class II restricted T cell epitope (MHC-II
 CC epitope) derived from the cancer antigen, NY ESO-1. The MHC-II epitopes
 CC from NY ESO-1 are recognised by CD4+ T lymphocytes in an human leukocyte
 CC antigen (HLA) class II restricted manner, in particular HLA-DR or HLA-DP
 CC restricted. The products of the gene are promising candidates for
 CC immunotherapeutic strategies for the prevention, treatment and diagnosis
 CC of patients with cancer. The cancer epitopes are useful as immunogen and
 CC vaccine to inhibit or to prevent cancer in a mammal by eliciting CD4+ T
 CC lymphocytes resulting in protection of the recipient from development of
 CC cancer and protection from metastasis, or by inhibiting the growth of
 CC cells expressing the NY-ESO-1 gene product. The cancer peptides are also
 CC useful as diagnostic agent to detect the presence of cancer, to enhance
 CC the generation of antibody and/or CD8+ T cell responses against any given
 CC target antigen and/or hapten and to induce tumour-specific humoral-
 CC mediated immunity against cancer. The present sequence is human NY ESO-1
 CC peptide used in the characterisation of the NY ESO-1 epitope recognised
 CC by TE4-1

XX Sequence 14 AA;

XX Query Match 100.0%; Score 47; DB 4; Length 14;

Best Local Similarity 100.0%; Pred. No. 0.0053;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TVSGNLTIR 10
| | | | | | | | | |
Db 4 TVSGNLTIR 13

RESULT 4
AAE07728
ID AAE07728 standard; peptide; 14 AA.
XX
AC AAE07728;
XX
DT 06-NOV-2001 (first entry)
XX
DE Human NY ESO-1 MHC class II restricted T cell epitope #14.
XX
KW Human; major histocompatibility complex; MHC; vaccine; metastasis;
KW class II restricted T cell epitope; MHC-II epitope; cancer antigen;
KW NY ESO-1 protein; CD4+ T lymphocyte; human leucocyte antigen; HLA;
KW tumour-specific humoral-mediated immunity; cancer; cytostatic;
KW immunotherapy.
XX
OS Homo sapiens.
XX
PN WO200155393-A2.
XX
PD 02-AUG-2001.
XX
PF 26-JAN-2001; 2001WO-US002765.
XX
PR 28-JAN-2000; 2000US-0179004P.
PR 29-SEP-2000; 2000US-0237107P.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Wang R, Rosenberg SA, Zeng G;
XX
DR WPI; 2001-496851/54.
XX
PT New NY-ESO cancer peptide or MHC class II restricted T cell epitopes,
PT useful as immunogen and vaccine for inhibiting cancer in a mammal or as
PT protection from metastasis.
XX
PS Claim 4; Page 16; 134pp; English.
XX
CC The invention relates to the identification and isolation of major
CC histocompatibility (MHC) class II restricted T cell epitope (MHC-II
CC epitope) derived from the cancer antigen, NY ESO-1. The MHC-II epitopes
CC from NY ESO-1 are recognised by CD4+ T lymphocytes in an human leucocyte
CC antigen (HLA) class II restricted manner, in particular HLA-DR or HLA-DP
CC restricted. The products of the gene are promising candidates for
CC immunotherapeutic strategies for the prevention, treatment and diagnosis
CC of patients with cancer. The cancer epitopes are useful as immunogen and
CC vaccine to inhibit or to prevent cancer in a mammal by eliciting CD4+ T
CC lymphocytes resulting in protection of the recipient from development of
CC cancer and protection from metastasis, or by inhibiting the growth of
CC cells expressing the NY-ESO-1 gene product. The cancer peptides are also
CC useful as diagnostic agent to detect the presence of cancer, to enhance
CC the generation of antibody and/or CD8+ T cell responses against any given
CC target antigen and/or hapten and to induce tumour-specific humoral-
CC mediated immunity against cancer. The present sequence is MHC class II
CC restricted T cell epitope of human NY ESO-1 protein
XX
SQ Sequence 14 AA;

Query Match 100.0%; Score 47; DB 4; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.0053;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TVSGNLTIR 10
| | | | | | | | | |

Db 4 TVSGNLTIR 13

RESULT 5
AAE07726
ID AAE07726 standard; peptide; 15 AA.
XX
AC AAE07726;
XX
DT 06-NOV-2001 (first entry)
XX
DE Human NY ESO-1 MHC class II restricted T cell epitope #12.
XX
KW Human; major histocompatibility complex; MHC; vaccine; metastasis;
KW class II restricted T cell epitope; MHC-II epitope; cancer antigen;
KW NY ESO-1 protein; CD4+ T lymphocyte; human leucocyte antigen; HLA;
KW tumour-specific humoral-mediated immunity; cancer; cytostatic;
KW immunotherapy.
XX
OS Homo sapiens.
XX
PN WO200155393-A2.
XX
PD 02-AUG-2001.
XX
PF 26-JAN-2001; 2001WO-US002765.
XX
PR 28-JAN-2000; 2000US-0179004P.
PR 29-SEP-2000; 2000US-0237107P.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Wang R, Rosenberg SA, Zeng G;
XX
DR WPI; 2001-496851/54.
XX
PT New NY-ESO cancer peptide or MHC class II restricted T cell epitopes,
PT useful as immunogen and vaccine for inhibiting cancer in a mammal or as
PT protection from metastasis.
XX
PS Claim 4; Page 16; 134pp; English.
XX
CC The invention relates to the identification and isolation of major
CC histocompatibility (MHC) class II restricted T cell epitope (MHC-II
CC epitope) derived from the cancer antigen, NY ESO-1. The MHC-II epitopes
CC from NY ESO-1 are recognised by CD4+ T lymphocytes in an human leucocyte
CC antigen (HLA) class II restricted manner, in particular HLA-DR or HLA-DP
CC restricted. The products of the gene are promising candidates for
CC immunotherapeutic strategies for the prevention, treatment and diagnosis
CC of patients with cancer. The cancer epitopes are useful as immunogen and
CC vaccine to inhibit or to prevent cancer in a mammal by eliciting CD4+ T
CC lymphocytes resulting in protection of the recipient from development of
CC cancer and protection from metastasis, or by inhibiting the growth of
CC cells expressing the NY-ESO-1 gene product. The cancer peptides are also
CC useful as diagnostic agent to detect the presence of cancer, to enhance
CC the generation of antibody and/or CD8+ T cell responses against any given
CC target antigen and/or hapten and to induce tumour-specific humoral-
CC mediated immunity against cancer. The present sequence is MHC class II
CC restricted T cell epitope of human NY ESO-1 protein
XX
SQ Sequence 15 AA;

Query Match 100.0%; Score 47; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.0058;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TVSGNLTIR 10
| | | | | | | | | |
Db 6 TVSGNLTIR 15

RESULT 6
AAE07727

ID AAE07727 standard; peptide; 15 AA.
 XX AC AAE07727;
 XX DT 06-NOV-2001 (first entry)
 XX DE Human NY ESO-1 MHC class II restricted T cell epitope #13.
 XX KW Human; major histocompatibility complex; MHC; vaccine; metastasis;
 KW class II restricted T cell epitope; MHC-II epitope; cancer antigen;
 KW NY ESO-1 protein; CD4+ T lymphocyte; human leucocyte antigen; HLA;
 KW tumour-specific humoral-mediated immunity; cancer; cytostatic;
 KW immunotherapy.
 XX OS Homo sapiens.
 XX PN WO200155393-A2.
 XX PD 02-AUG-2001.
 XX PF 26-JAN-2001; 2001WO-US002765.
 XX PR 28-JAN-2000; 2000US-0179004P.
 XX PR 29-SEP-2000; 2000US-0237107P.
 XX PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX PI Wang R, Rosenberg SA, Zeng G;
 XX PI WPI; 2001-496851/54.
 XX PT New NY-ESO cancer peptide or MHC class II restricted T cell epitopes,
 PT useful as immunogen and vaccine for inhibiting cancer in a mammal or as
 PT protection from metastasis.
 XX PS Claim 4; Page 16; 134pp; English.
 CC The invention relates to the identification and isolation of major
 CC histocompatibility (MHC) class II restricted T cell epitope (MHC-II
 CC epitope) derived from the cancer antigen, NY ESO-1. The MHC-II epitopes
 CC from NY ESO-1 are recognised by CD4+ T lymphocytes in an human leucocyte
 CC antigen (HLA) class II restricted manner, in particular HLA-DR or HLA-DP
 CC restricted. The products of the gene are promising candidates for
 CC immunotherapeutic strategies for the prevention, treatment and diagnosis
 CC of patients with cancer. The cancer epitopes are useful as immunogen and
 CC vaccine to inhibit or to prevent cancer in a mammal by eliciting CD4+ T
 CC lymphocytes resulting in protection of the recipient from development of
 CC cancer and protection from metastasis, or by inhibiting the growth of
 CC cells expressing the NY-ESO-1 gene product. The cancer peptides are also
 CC useful as diagnostic agent to detect the presence of cancer, to enhance
 CC the generation of antibody and/or CD8+ T cell responses against any given
 CC target antigen and/or hapten and to induce tumour-specific humoral-
 CC mediated immunity against cancer. The present sequence is MHC class II
 CC restricted T cell epitope of human NY ESO-1 protein

XX SQ Sequence 15 AA;
 Query Match 100.0%; Score 47; DB 4; Length 15;
 Best Local Similarity 100.0%; Pred. No. 0.0058;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TVSGNLTIR 10
 |||||
 Db 5 TVSGNLTIR 14

RESULT 7
 AAE07786
 ID AAE07786 standard; peptide; 15 AA.
 XX AC AAE07786;
 XX DT 06-NOV-2001 (first entry)

XX DE Human NY ESO-1 peptide #20 to characterise epitope recognised by TE4-1.
 XX KW Human; major histocompatibility complex; MHC; vaccine; metastasis;
 KW class II restricted T cell epitope; MHC-II epitope; cancer antigen;
 KW NY ESO-1 protein; CD4+ T lymphocyte; human leucocyte antigen; HLA;
 KW tumour-specific humoral-mediated immunity; cancer; cytostatic;
 KW immunotherapy.
 XX OS Homo sapiens.
 XX PN WO200155393-A2.
 XX PD 02-AUG-2001.
 XX PF 26-JAN-2001; 2001WO-US002765.
 XX PR 28-JAN-2000; 2000US-0179004P.
 XX PR 29-SEP-2000; 2000US-0237107P.
 XX PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX PI Wang R, Rosenberg SA, Zeng G;
 XX PI WPI; 2001-496851/54.
 XX PT New NY-ESO cancer peptide or MHC class II restricted T cell epitopes,
 PT useful as immunogen and vaccine for inhibiting cancer in a mammal or as
 PT protection from metastasis.
 XX PS Example 6; Fig 6A; 134pp; English.
 CC The invention relates to the identification and isolation of major
 CC histocompatibility (MHC) class II restricted T cell epitope (MHC-II
 CC epitope) derived from the cancer antigen, NY ESO-1. The MHC-II epitopes
 CC from NY ESO-1 are recognised by CD4+ T lymphocytes in an human leucocyte
 CC antigen (HLA) class II restricted manner, in particular HLA-DR or HLA-DP
 CC restricted. The products of the gene are promising candidates for
 CC immunotherapeutic strategies for the prevention, treatment and diagnosis
 CC of patients with cancer. The cancer epitopes are useful as immunogen and
 CC vaccine to inhibit or to prevent cancer in a mammal by eliciting CD4+ T
 CC lymphocytes resulting in protection of the recipient from development of
 CC cancer and protection from metastasis, or by inhibiting the growth of
 CC cells expressing the NY-ESO-1 gene product. The cancer peptides are also
 CC useful as diagnostic agent to detect the presence of cancer, to enhance
 CC the generation of antibody and/or CD8+ T cell responses against any given
 CC target antigen and/or hapten and to induce tumour-specific humoral-
 CC mediated immunity against cancer. The present sequence is human NY ESO-1
 CC peptide used in the characterisation of the NY ESO-1 epitope recognised
 CC by TE4-1

XX SQ Sequence 15 AA;
 Query Match 100.0%; Score 47; DB 4; Length 15;
 Best Local Similarity 100.0%; Pred. No. 0.0058;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TVSGNLTIR 10
 |||||
 Db 6 TVSGNLTIR 15

RESULT 8
 AAE07787
 ID AAE07787 standard; peptide; 15 AA.
 XX AC AAE07787;
 XX DT 06-NOV-2001 (first entry)
 XX DE Human NY ESO-1 peptide #21 to characterise epitope recognised by TE4-1.
 XX KW Human; major histocompatibility complex; MHC; vaccine; metastasis;

KW class II restricted T cell epitope; MHC-II epitope; cancer antigen;
 KW NY ESO-1 protein; CD4+ T lymphocyte; human leukocyte antigen; HLA;
 KW tumour-specific humoral-mediated immunity; cancer; cytostatic;
 KW immunotherapy.
 XX
 OS Homo sapiens.
 XX
 PN WO200155393-A2.
 XX
 PD 02-AUG-2001.
 XX
 PF 26-JAN-2001; 2001WO-US002765.
 XX
 XX 28-JAN-2000; 2000US-0179004P.
 PR 29-SEP-2000; 2000US-0237107P.
 XX
 XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
 PA
 XX Wang R, Rosenberg SA, Zeng G;
 PI WPI; 2001-496851/54.
 XX
 DR New NY-ESO cancer peptide or MHC class II restricted T cell epitopes,
 XX useful as immunogen and vaccine for inhibiting cancer in a mammal or as
 PT protection from metastasis.
 XX
 PS Example 6; Fig 6A; 134pp; English.
 XX
 CC The invention relates to the identification and isolation of major
 CC histocompatibility (MHC) class II restricted T cell epitope (MHC-II
 CC epitope) derived from the cancer antigen, NY ESO-1. The MHC-II epitopes
 CC from NY ESO-1 are recognised by CD4+ T lymphocytes in an human leukocyte
 CC antigen (HLA) class II restricted manner, in particular HLA-DR or HLA-DP
 CC restricted. The products of the gene are promising candidates for
 CC immunotherapeutic strategies for the prevention, treatment and diagnosis
 CC of patients with cancer. The cancer epitopes are useful as immunogen and
 CC vaccine to inhibit or to prevent cancer in a mammal by eliciting CD4+ T
 CC lymphocytes resulting in protection of the recipient from development of
 CC cancer and protection from metastasis, or by inhibiting the growth of
 CC cells expressing the NY-ESO-1 gene product. The cancer peptides are also
 CC useful as diagnostic agent to detect the presence of cancer, to enhance
 CC the generation of antibody and/or CD8+ T cell responses against any given
 CC target antigen and/or hapten and to induce tumour-specific humoral-
 CC mediated immunity against cancer. The present sequence is human NY ESO-1
 CC peptide used in the characterisation of the NY ESO-1 epitope recognised
 CC by TE4-1
 XX
 SQ Sequence 15 AA;
 Query Match 100.0%; Score 47; DB 4; Length 15;
 Best Local Similarity 100.0%; Pred. No. 0.0058;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TVSGNLTIR 10
 DB 5 TVSGNLTIR 14
 |||||
 RESULT 9
 AAY52440
 ID AAY52440 standard; protein; 18 AA.
 XX
 AC AAY52440;
 XX
 XX 15-FEB-2000 (first entry)
 DT
 XX Human tumour antigen NY-ESO-1 peptide #13.
 DE
 DE Cancer; tumour; antigen; MHC; major histocompatibility complex; Class II;
 KW T-cell; helper; stimulation; proliferation; treatment; diagnosis;
 KW prevention; melanoma; breast cancer; ovarian cancer; prostate cancer;
 KW hepatoma; thyroid cancer; bladder cancer; lung cancer; lymphoma.
 XX

OS Synthetic.
 OS Homo sapiens.
 PN WO9953938-A1.
 XX
 PD 28-OCT-1999.
 XX
 PF 24-MAR-1999; 99WO-US006875.
 XX
 PR 17-APR-1998; 98US-00062422.
 PR 02-OCT-1998; 98US-00165546.
 XX
 PA (LUDW-) LUDWIG INST CANCER RES.
 XX
 XX Stockert E, Jager E, Chen Y, Scanlan M, Alexander K, Old LJ;
 PI Gure A, Ritter G;
 XX WPI; 2000-038483/03.
 DR
 XX Novel peptides which bind to MHC class I and MHC class II molecules,
 PT useful for therapeutic and diagnostic purposes.
 XX
 PS Claim 4; Page 22; 49pp; English.
 XX
 CC Peptides #8-13 (AAY52435-Y52440) are peptides derived from the human
 CC tumour antigen, NY-ESO-1 (AAY52430) which can bind to MHC(major
 CC histocompatibility Class II HLA-DR53 molecules, thereby stimulating
 CC proliferation of helper T-cells. cDNA encoding NY-ESO-1 was initially
 CC isolated from an oesophagus squamous cell cancer cDNA library. Tissue
 CC localisation studies revealed it to be expressed at high levels in normal
 CC ovary and testis but not in normal colon, kidney, liver, brain,
 CC oesophagus and skin. It was expressed in certain tumours and tumour cell
 CC lines with some degree of frequency - these included melanoma specimens
 CC and cell lines, and breast and bladder cancer specimens, with expression
 CC in other tumour types being sporadic. These NY-ESO-1-derived peptides may
 CC be used in methods and compositions used for the treatment, diagnosis and
 CC prevention of cancers (such as melanoma, breast cancer, prostate cancer,
 CC lung cancer, hepatoma, ovarian cancer, thyroid cancer, bladder cancer, or
 CC lymphoma) and to stimulate the proliferation of T cells
 XX
 SQ Sequence 18 AA;
 Query Match 100.0%; Score 47; DB 3; Length 18;
 Best Local Similarity 100.0%; Pred. No. 0.0073;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TVSGNLTIR 10
 DB 1 TVSGNLTIR 10
 |||||
 RESULT 10
 AAB69940
 ID AAB69940 standard; peptide; 18 AA.
 XX
 AC AAB69940;
 XX
 XX 27-APR-2001 (first entry)
 DT
 XX Human NY-ESO-1 HLA-DR53 binding motif #2.
 DE
 DE Human; NY-ESO-1; HLA; human leukocyte antigen; CTL; cytotoxic T cell;
 KW HLA-A2; HLA-DR53; melanoma; adenocarcinoma; bladder carcinoma;
 KW non-small cell lung carcinoma; tumour status determination.
 XX
 OS Homo sapiens.
 XX
 PN WO200107917-A1.
 XX
 PD 01-FEB-2001.
 XX
 XX 14-JUL-2000; 2000WO-US019220.
 XX

PR 23-JUL-1999; 99US-00359503.
 XX (LUDW-) LUDWIG INST CANCER RES.
 PA (SLOK) SLOAN KETTERING INST CANCER RES.
 XX (CORR) CORNELL RES FOUND INC.
 XX
 PI Jager E, Stockert E, Old LJ, Knuth A, Chen Y, Scanlan M;
 XX WPI; 2001-182822/18.
 DR
 XX
 XX Method useful for determining the status (e.g. progression, regression or
 PT stability of the disease) of a cancerous condition, involves determining
 PT the levels of NY-ESO-1 specific antibodies in a sample taken from a
 PT patient.
 XX
 XX Example 16; Page 27; 50pp; English.
 PS
 XX The present sequence is given in a specification relating to a method for
 XX determining the status of a cancerous condition in a patient with a
 CC tumour that expresses NY-ESO-1. The method comprises assaying a sample
 CC taken from the patient for antibodies that specifically bind to the NY-
 CC ESO-1 and comparing the value obtained to a prior value obtained from
 CC assay of a prior sample taken from the patient. Any difference between
 CC the values is indicative of a change in status of the cancerous
 CC condition. The method is useful for determining whether a cancerous
 CC condition is progressing, regressing or remaining stable, in particular
 CC in patients receiving treatment for a melanoma, adenocarcinoma, non-small
 CC cell lung carcinoma or bladder carcinoma
 XX
 XX Sequence 18 AA;
 SQ
 Query Match 100.0%; Score 47; DB 4; Length 18;
 Best Local Similarity 100.0%; Pred. No. 0.0073;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TVSGNLTIR 10
 Db 7 TVSGNLTIR 16
 RESULT 11
 AAB69944
 ID AAB69944 standard; peptide; 18 AA.
 XX
 AC AAB69944;
 XX
 XX 27-APR-2001 (first entry)
 DT
 XX
 XX Human NY-ESO-1 HLA-DR53 binding motif #6.
 DE
 XX Human; NY-ESO-1; HLA; human leukocyte antigen; CTL; cytotoxic T cell;
 KW HLA-A2; HLA-DR53; melanoma; adenocarcinoma; bladder carcinoma;
 KW non-small cell lung carcinoma; tumour status determination.
 XX
 XX Homo sapiens.
 OS
 XX WO200107917-A1.
 PN
 XX 01-FEB-2001.
 PD
 XX
 XX 14-JUL-2000; 2000WO-US019220.
 PF
 XX 23-JUL-1999; 99US-00359503.
 PR
 XX (LUDW-) LUDWIG INST CANCER RES.
 PA (SLOK) SLOAN KETTERING INST CANCER RES.
 XX (CORR) CORNELL RES FOUND INC.
 XX
 XX Jager E, Stockert E, Old LJ, Knuth A, Chen Y, Scanlan M;
 PI WPI; 2001-182822/18.
 XX
 XX Method useful for determining the status (e.g. progression, regression or

PT stability of the disease) of a cancerous condition, involves determining
 PT the levels of NY-ESO-1 specific antibodies in a sample taken from a
 PT patient.
 XX
 XX Example 16; Page 28; 50pp; English.
 XX
 CC The present sequence is given in a specification relating to a method for
 CC determining the status of a cancerous condition in a patient with a
 CC tumour that expresses NY-ESO-1. The method comprises assaying a sample
 CC taken from the patient for antibodies that specifically bind to the NY-
 CC ESO-1 and comparing the value obtained to a prior value obtained from
 CC assay of a prior sample taken from the patient. Any difference between
 CC the values is indicative of a change in status of the cancerous
 CC condition. The method is useful for determining whether a cancerous
 CC condition is progressing, regressing or remaining stable, in particular
 CC in patients receiving treatment for a melanoma, adenocarcinoma, non-small
 CC cell lung carcinoma or bladder carcinoma
 XX
 XX Sequence 18 AA;
 SQ
 Query Match 100.0%; Score 47; DB 4; Length 18;
 Best Local Similarity 100.0%; Pred. No. 0.0073;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TVSGNLTIR 10
 Db 1 TVSGNLTIR 10
 RESULT 12
 AAU01544
 ID AAU01544 standard; peptide; 18 AA.
 XX
 AC AAU01544;
 XX
 XX 18-JUL-2001 (first entry)
 DT
 XX
 XX HLA-DR53 recognising NY-ESO-1 peptide #6.
 DE
 XX NY-ESO-1; human; tumour rejection antigen precursor; SSX-2; MHC Class II;
 KW major histocompatibility complex; helper T cell; HLA-DR; cancer;
 KW human leukocyte antigen-determining region; disease progression;
 KW disease regression; disease onset; body tissue; body fluid; enzyme label;
 KW radioactive label; monoclonal antibody.
 XX
 XX Homo sapiens.
 OS
 XX WO200123560-A2.
 PN
 XX 05-APR-2001.
 PD
 XX 26-SEP-2000; 2000WO-US026411.
 PF
 XX 29-SEP-1999; 99US-00408036.
 PR
 XX (LUDW-) LUDWIG INST CANCER RES.
 PA
 XX Tureci O, Sahin U, Pfreundschuh M;
 PI WPI; 2001-366156/27.
 XX
 XX Polypeptides binding to major histocompatibility complex class II human
 PT leukocyte antigen-determining region molecule having amino acid sequence
 PT found in tumor rejection antigen precursor used for stimulating
 PT proliferation of helper T cells.
 XX
 XX Example 13; Page 19; 62pp; English.
 PS
 XX The sequence represents a human NY-ESO-1 tumour rejection antigen
 CC precursor fragment which recognises and binds to HLA-DR53. NY-ESO-1 and
 CC SSX-2 polypeptides, or fragments of, bind to major histocompatibility
 CC complex (MHC) Class II molecules such as human leukocyte antigen-
 CC determining region (HLA-DR) molecules and stimulate proliferation of

CC helper T cells. The peptides can be administered to an HLA-DR positive
 CC subject in order to stimulate the helper T cells. An MHC Class II HLA-DR-
 CC NY-ESO-1/SSX-2 complex expressed on the surface of a cell or present in
 CC free form is useful for this stimulation. The nucleic acid is useful for
 CC screening for a cancerous condition, which involves contacting a subject
 CC sample to a cell line transfected with the immunoreactive cell (helper T
 CC cell), where interaction is indicative of cancer. In addition, a sample
 CC from a patient (for example, a body fluid or tissue) can be monitored for
 CC determining regression, progression or onset of a cancerous condition.
 CC The method involves contacting the sample with a radioactive labelled or
 CC enzyme labelled monoclonal antibody which specifically binds with the
 CC complex

XX Sequence 18 AA;
 CC Query Match 100.0%; Score 47; DB 4; Length 18;
 CC Best Local Similarity 100.0%; Pred. No. 0.0073;
 CC Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TVSGNLTIR 10
 DB 1 TVSGNLTIR 10
 |||||

RESULT 13
 AAU01540
 ID AAU01540 standard; peptide; 18 AA.

XX AAU01540;
 XX 19-JUL-2001 (first entry)
 XX HLA-DR53 recognising NY-ESO-1 peptide #2.
 XX NY-ESO-1; human; tumour rejection antigen precursor; SSX-2; MHC Class II;
 KW major histocompatibility complex; helper T cell; HLA-DR; cancer;
 KW human leukocyte antigen-determining region; disease progression;
 KW disease regression; disease onset; body tissue; body fluid; enzyme label;
 KW radioactive label; monoclonal antibody.

XX Homo sapiens.

XX WO200123560-A2.

XX 05-APR-2001.

XX 26-SEP-2000; 2000WO-US026411.

XX 29-SEP-1999; 99US-00408036.

XX (LUDW-) LUDWIG INST CANCER RES.

XX Tureci O, Sahin U, Pfreundschuh M;

XX WPI; 2001-266156/27.

XX Polypeptides binding to major histocompatibility complex class II human
 CC leukocyte antigen-determining region molecule having amino acid sequence
 CC found in tumor rejection antigen precursor used for stimulating
 CC proliferation of helper T cells.

XX Example 13; Page 19; 62pp; English.

XX The sequence represents a human NY-ESO-1 tumour rejection antigen
 CC precursor fragment which recognises and binds to HLA-DR53. NY-ESO-1 and
 CC SSX-2 polypeptides, or fragments of, bind to major histocompatibility
 CC complex (MHC) Class II molecules such as human leukocyte antigen-
 CC determining region (HLA-DR) molecules and stimulate proliferation of
 CC helper T cells. The peptides can be administered to an HLA-DR positive
 CC subject in order to stimulate the helper T cells. An MHC Class II HLA-DR-
 CC NY-ESO-1/SSX-2 complex expressed on the surface of a cell or present in
 CC free form is useful for this stimulation. The nucleic acid is useful for

CC screening for a cancerous condition, which involves contacting a subject
 CC sample to a cell line transfected with the immunoreactive cell (helper T
 CC cell), where interaction is indicative of cancer. In addition, a sample
 CC from a patient (for example, a body fluid or tissue) can be monitored for
 CC the amount of the complex present in the bloodstream. This is useful for
 CC determining regression, progression or onset of a cancerous condition.
 CC The method involves contacting the sample with a radioactive labelled or
 CC enzyme labelled monoclonal antibody which specifically binds with the
 CC complex

XX Sequence 18 AA;

CC Query Match 100.0%; Score 47; DB 4; Length 18;
 CC Best Local Similarity 100.0%; Pred. No. 0.0073;
 CC Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TVSGNLTIR 10
 DB 7 TVSGNLTIR 16
 |||||

RESULT 14
 AAE07769
 ID AAE07769 standard; peptide; 18 AA.

XX AAE07769;

XX 06-NOV-2001 (first entry)

XX Human NY ESO-1 HLA DR restricted T cell cancer peptide #1.

XX Human; major histocompatibility complex; MHC; vaccine; metastasis;
 KW class II restricted T cell epitope; MHC-II epitope; cancer antigen;
 KW NY ESO-1 protein; CD4+ T lymphocyte; human leukocyte antigen; HLA;
 KW tumour-specific humoral-mediated immunity; cancer; cytostatic;
 KW immunotherapy.

XX Homo sapiens.

XX WO200155393-A2.

XX 02-AUG-2001.

XX 26-JAN-2001; 2001WO-US002765.

XX 28-JAN-2000; 2000US-0179004P.

XX 29-SEP-2000; 2000US-0237107P.

XX (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX Wang R, Rosenberg SA, Zeng G;

XX WPI; 2001-496851/54.

XX New NY-ESO cancer peptide or MHC class II restricted T cell epitopes,
 CC useful as immunogen and vaccine for inhibiting cancer in a mammal or as
 CC protection from metastasis.

XX Claim 84; Page 84; 134pp; English.

XX The invention relates to the identification and isolation of major
 CC histocompatibility (MHC) class II restricted T cell epitope (MHC-II
 CC epitope) derived from the cancer antigen, NY ESO-1. The MHC-II epitopes
 CC from NY ESO-1 are recognised by CD4+ T lymphocytes in an human leukocyte
 CC antigen (HLA) class II restricted manner, in particular HLA-DR or HLA-DP
 CC restricted. The products of the gene are promising candidates for
 CC immunotherapeutic strategies for the prevention, treatment and diagnosis
 CC of patients with cancer. The cancer epitopes are useful as immunogen and
 CC vaccine to inhibit or to prevent cancer in a mammal by eliciting CD4+ T
 CC lymphocytes resulting in protection of the recipient from development of
 CC cancer and protection from metastasis, or by inhibiting the growth of
 CC cells expressing the NY-ESO-1 gene product. The cancer peptides are also
 CC useful as diagnostic agent to detect the presence of cancer, to enhance

CC the generation of antibody and/or CD8+ T cell responses against any given
CC target antigen and/or hapten and to induce tumour-specific humoral-
CC mediated immunity against cancer. The present sequence is human NY ESO-1
CC HLA DR restricted T cell cancer peptide

XX
SQ Sequence 18 AA;

Query Match 100.0%; Score 47; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 0.0073;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TVSGNLTIR 10
|||
Db 7 TVSGNLTIR 16

RESULT 15
AAE07742
ID AAE07742 standard; peptide; 20 AA.

AC AAE07742;

DT 06-NOV-2001 (first entry)

DE Human ESO p126-145 peptide, to identify MHC class II-restricted epitopes.

XX Human; major histocompatibility complex; MHC; vaccine; metastasis;
KW class II restricted T cell epitope; MHC-II epitope; cancer antigen;
KW NY ESO-1 protein; CD4+ T lymphocyte; human leucocyte antigen; HLA;
KW tumour-specific humoral-mediated immunity; cancer; cytostatic;
KW immunotherapy.

XX Homo sapiens.

XX WO200155393-A2.

XX 02-AUG-2001.

XX 26-JAN-2001; 2001WO-US002765.

XX 28-JAN-2000; 2000US-0179004P.

XX 29-SEP-2000; 2000US-0237107P.

XX (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX Wang R, Rosenberg SA, Zeng G;

XX WPI; 2001-496851/54.

XX New NY-ESO cancer peptide or MHC class II restricted T cell epitopes,
PT useful as immunogen and vaccine for inhibiting cancer in a mammal or as
PT protection from metastasis.

XX Example 3; Fig 3; 134pp; English.

XX The invention relates to the identification and isolation of major
CC histocompatibility (MHC) class II restricted T cell epitope (MHC-II
CC epitope) derived from the cancer antigen, NY ESO-1. The MHC-II epitopes
CC from NY ESO-1 are recognised by CD4+ T lymphocytes in an human leucocyte
CC antigen (HLA) class II restricted manner, in particular HLA-DR or HLA-DP
CC restricted. The products of the gene are promising candidates for
CC immunotherapeutic strategies for the prevention, treatment and diagnosis
CC of patients with cancer. The cancer epitopes are useful as immunogen and
CC vaccine to inhibit or to prevent cancer in a mammal by eliciting CD4+ T
CC lymphocytes resulting in protection of the recipient from development of
CC cancer and protection from metastasis, or by inhibiting the growth of
CC cells expressing the NY-ESO-1 gene product. The cancer peptides are also
CC useful as diagnostic agent to detect the presence of cancer, to enhance
CC the generation of antibody and/or CD8+ T cell responses against any given
CC target antigen and/or hapten and to induce tumour-specific humoral-
CC mediated immunity against cancer. The present sequence is human ESO p126-
CC 145 peptide used in the identification of putative MHC class II -
CC restricted epitopes from HLA-DR4-transgenic mice

XX
SQ Sequence 20 AA;

Query Match 100.0%; Score 47; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.0084;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TVSGNLTIR 10
|||
Db 2 TVSGNLTIR 11

Search completed: September 11, 2005, 01:38:05
Job time : 15.3333 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 11, 2005, 01:28:54 ; Search time 2.80952 Seconds
(without alignments)
342.466 Million cell updates/sec.

Title: US-09-529-206E-4_COPY_127_136

Perfect score: 47

Sequence: 1 TVSGNLTITR 10

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR 79.*

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	36	76.6	245	2 T13099	major tail protein
2	36	76.6	323	2 AD2753	lipic Acid Synthetase
3	36	76.6	323	2 B97534	lipic acid synthetase
4	35	74.5	335	2 A89837	hypothetical protein
5	34	72.3	177	1 R5BS0F	ribosomal protein
6	34	72.3	244	2 T41234	translation initiation
7	34	72.3	311	2 AB3218	2-hydroxyacid dehydrogenase
8	34	72.3	314	2 G86035	hypothetical protein
9	34	72.3	1266	2 A85989	hypothetical protein
10	34	72.3	1266	2 F91143	hypothetical protein
11	33	70.2	144	1 TPBPPI	tail fiber protein
12	33	70.2	144	2 S18683	gene R protein - E
13	33	70.2	411	2 G95241	MATE efflux family
14	33	70.2	426	2 B98106	hypothetical protein
15	33	70.2	428	2 F85253	hypothetical protein
16	33	70.2	436	2 B81033	N-acetylglutamate
17	33	70.2	436	2 A81977	probable amino-acyl transferase
18	33	70.2	449	2 S02011	serotonin receptor
19	33	70.2	471	2 A43956	serotonin receptor
20	33	70.2	471	2 S11280	serotonin receptor
21	33	70.2	471	2 S40589	5-hydroxytryptamin
22	33	70.2	471	2 A34863	serotonin receptor
23	33	70.2	876	2 E96574	hypothetical protein
24	33	70.2	918	2 T02759	hypothetical protein
25	33	70.2	1996	2 F71405	probable TWV resist
26	32	68.1	102	2 C86898	hypothetical protein
27	32	68.1	121	2 B81972	probable integral
28	32	68.1	135	2 D81029	conserved hypothet
29	32	68.1	187	2 I37105	5-Htrc receptor -

30 32 68.1 234 2 H75390 hypothetical prote
31 32 68.1 245 2 S57550 hypothetical prote
32 32 68.1 289 2 C87158 probable oxidoredu
33 32 68.1 316 2 S25234 lysozyme (EC 3.2.1
34 32 68.1 344 2 A69325 hypothetical prote
35 32 68.1 347 2 G95146 conserved domain p
36 32 68.1 347 2 E98014 conserved hypothet
37 32 68.1 376 2 C97059 uncharacterized pr
38 32 68.1 418 2 E70401 s-adenosylhomocyst
39 32 68.1 451 2 S65162 hypothetical prote
40 32 68.1 455 1 HMXRS3 sigma 1 protein pr
41 32 68.1 458 2 JS0616 serotonin receptor
42 32 68.1 459 2 A43951 serotonin receptor
43 32 68.1 460 2 A32605 serotonin receptor
44 32 68.1 479 2 S23562 serotonin receptor
45 32 68.1 491 2 T30590 alkylhalidase homo

ALIGNMENTS

RESULT 1

T13099

major tail protein V - phage N15

N;Alternate names: protein gp13

C:Species: phage N15

C>Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 09-Jul-2004

C:Accession: T13099

R:Hendrix, R.W.; Ravin, V.K.; Casjens, S.R.; Ford, M.E.; Ravin, N.V.; Smirnov, I.K.

submitted to the EMBL Data Library, May 1998

A:Reference number: Z17603

A:Accession: T13099

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-245 <HEND>

A:Cross-references: UNIPROT:O64327; EMBL:AF064539; NID:G3192683; PID:G3192697; PIDN:AAC

C:Genetics:

A>Note: Gene 13

C:Superfamily: phage lambda major tail protein V

Query Match 76.6%; Score 36; DB 2; Length 245;
Best Local Similarity 77.8%; Pred. No. 14;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 TVSGNLTIT 9

Db 209 TVSGNLTITV 217

RESULT 2

AD2753

lipic Acid Synthetase [imported] - Agrobacterium tumefaciens (strain C58, Dupont)

C:Species: Agrobacterium tumefaciens

C>Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004

C:Accession: AD2753

R:Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, Y.

erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutyavin, T.; Levy, R.; Li, M.; McClellan

; Karp, P.; Romero, P.; Zhang, S.

Science 294, 2317-2323, 2001

A:Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,

ster, E.W.

A:Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.

A:Reference number: AB2577; MUID:21608550; PMID:11743193

A:Accession: AD2753

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-323 <KUR>

A:Cross-references: UNIPROT:Q8UGF1; GB:AE008688; PIDN:AAL42442.1; PID:gl7739856; GSPDB:

A:Experimental source: strain C58 (Dupont)

C:Genetics:

A:Gene: lipA

A:Map position: circular chromosome

C:Superfamily: lipic acid synthase

Query Match 76.6%; Score 36; DB 2; Length 323;
 Best Local Similarity 70.0%; Pred. No. 18;
 Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 TVSGNLTIR 10

DB 189 TVFGNLTVR 198

RESULT 3

B97534

lipolic acid synthetase (lip-syn) (lipoate synthase) [imported] - Agrobacterium tumefaciens

C;Species: Agrobacterium tumefaciens

C;Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 09-Jul-2004

C;Accession: B97534

R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Quorllo, B.; Goldman,

A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.;

Science 294, 2323-2328, 2001

A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum

A;Reference number: A97359; MUID:21608551; PMID:11743194

A;Accession: B97534

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-323 <KUR>

A;Cross-references: UNIPROT:Q8UFG1; GB:AE007869; PIDN:AAK87227.1; PID:gl5156511; GSPDB:C

C;Genetics:

A;Gene: AGR_C_2646

A;Map position: circular chromosome

C;Superfamily: lipolic acid synthase

Query Match 76.6%; Score 36; DB 2; Length 323;
 Best Local Similarity 70.0%; Pred. No. 18;
 Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 TVSGNLTIR 10

DB 189 TVFGNLTVR 198

RESULT 4

A89837

hypothetical protein SA0619 [imported] - Staphylococcus aureus (strain N315)

C;Species: Staphylococcus aureus

C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004

C;Accession: A89837

R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Ogud

ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.;

C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.

Lancet 357, 1225-1240, 2001

A;Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.

A;Reference number: A89758; MUID:21311952; PMID:11418146

A;Accession: A89837

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-335 <KUR>

A;Cross-references: UNIPROT:Q99VW7; GB:BA000018; PID:gl3700555; PIDN:BA041852.1; GSPDB:C

A;Experimental source: strain N315

C;Genetics:

A;Gene: SA0619

C;Superfamily: probable sodium-dependent phosphate transporter MTH1885

Query Match 74.5%; Score 35; DB 2; Length 335;
 Best Local Similarity 70.0%; Pred. No. 30;
 Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 TVSGNLTIR 10

DB 245 TVGNIMKIR 254

RESULT 5

R5BS0F

2-hydroxyacid dehydrogenase Atu5474 [imported] - Agrobacterium tumefaciens (strain C58,

ribosomal protein L6 - Bacillus stearothermophilus

N;Alternate names: ribosomal protein BL10

C;Species: Bacillus stearothermophilus

C;Date: 02-Apr-1982 #sequence_revision 02-Apr-1982 #text_change 09-Jul-2004

C;Accession: A02766; B39085; S59061

R;Kimura, M.; Rawlings, N.; Appelt, K.

FEBS Lett. 136, 58-64, 1981

A;Title: The amino acid sequence of protein BL10 from the 50S subunit of the Bacillus st

A;Reference number: A02766

A;Accession: A02766

A;Molecule type: protein

A;Residues: 1-177 <KIM>

A;Cross-references: UNIPROT:P02391

R;Ramakrishnan, V.; Garckman, S.E.

J. Biol. Chem. 266, 880-885, 1991

A;Title: Cloning, sequencing, and overexpression of genes for ribosomal proteins from Ba

A;Reference number: A39085; MUID:91093287; PMID:1985969

A;Accession: B39085

A;Molecule type: DNA

A;Residues: 8-170 <RAM>

A;Cross-references: GB:M57622

R;Urlaub, H.; Kruff, V.; Bischof, O.; Mueller, E.C.; Wittmann-Liebold, B.

EMBO J. 14, 4578-4588, 1995

A;Title: Protein-rRNA binding features and their structural and functional implications

A;Reference number: S59051; MUID:96003638; PMID:7556101

A;Accession: S59061

A;Molecule type: protein

A;Residues: 149-163 <URL>

C;Superfamily: ribosomal protein L6/L9

C;Keywords: protein biosynthesis; ribosome

Query Match 72.3%; Score 34; DB 1; Length 177;

Best Local Similarity 55.6%; Pred. No. 25;

Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 TVSGNLTIR 9

DB 43 TVEGNVITV 51

RESULT 6

T41234

translation initiation factor eIF-6 [imported] - fission yeast (Schizosaccharomyces pom

C;Species: Schizosaccharomyces pombe

C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004

C;Accession: T41234

R;Lyne, M.; Harris, D.B.; Murphey, L.D.; Rajandream, M.A.; Barrell, B.G.

submitted to the EMBL Data Library, January 1999

A;Reference number: Z21979

A;Accession: T41234

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-244 <LYN>

A;Cross-references: UNIPROT:O94476; EMBL:AL035075; PIDN:CAA22640.1; GSPDB:GN00068; SPDB

A;Experimental source: strain 972h-; cosmid c1919

C;Genetics:

A;Gene: SPDB:SPCC1919.09

A;Map position: 3

A;Introns: 12/2; 36/2

C;Superfamily: conserved hypothetical protein YPR016c

Query Match 72.3%; Score 34; DB 2; Length 244;

Best Local Similarity 75.0%; Pred. No. 35;

Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 TVSGNLTIR 8

DB 141 TVAGNVLT 148

C;Species: Agrobacterium tumefaciens
C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004
C;Accession: AB3218
R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monke, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I.
erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutyavin, T.; Levy, R.; Li, M.; McClell
; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
ster, E.W.
A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A;Reference number: AB2577; MUID:21608550; PMID:11743193
A;Accession: AB3218
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-311 <KUR>
A;Cross-references: UNIPROT:Q8UJK3; GB:AE008687; PIDN:AAU46160.1; PID:gl7743930; GSPDB:
A;Experimental source: strain C58 (Dupont)
C;Genetics:
A;Gene: Atu5474
A;Genome: plasmid
C;Superfamily: phosphoglycerate dehydrogenase

Query Match 72.3%; Score 34; DB 2; Length 311;
Best Local Similarity 77.8%; Pred. No. 44;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 VSGNLTIR 10
:|||||
Db 288 VAGNLTIR 296

RESULT 8
G85835
hypothetical protein yreB [imported] - Lactococcus lactis subsp. lactis (strain IL1403)
C;Species: Lactococcus lactis subsp. lactis
C;Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 09-Jul-2004
C;Accession: G86835
R;Bolotin, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarne, K.; Weissenbach, J.; Ehrli
Genome Res. 11, 731-753, 2001
A;Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis s
A;Reference number: A86625; MUID:21235186; PMID:11337471
A;Accession: G86835
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-314 <STO>
A;Cross-references: UNIPROT:Q9CEZ4; GB:AE005176; PID:gl2724702; PIDN:AAK05785.1; GSPDB:
A;Experimental source: strain IL1403
C;Genetics:
A;Gene: yreB

Query Match 72.3%; Score 34; DB 2; Length 314;
Best Local Similarity 75.0%; Pred. No. 45;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 VSGNLTIR 9
:|||||
Db 93 ISGNLTIL 100

RESULT 9
A85989
hypothetical protein Z4604 [imported] - Escherichia coli (strain O157:H7, substrain EDL9
C;Species: Escherichia coli
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
C;Accession: A85989
R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca,
Nature 409, 529-533, 2001
A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A;Reference number: A85480; MUID:21074935; PMID:11206551
A;Accession: A85989
A;Status: preliminary
A;Molecule type: DNA

A;Residues: 1-1266 <STO>
A;Cross-references: UNIPROT:Q8X9D5; GB:AE005174; NID:gl2517869; PIDN:AAG58373.1; GSPDB:
A;Experimental source: strain O157:H7, substrain EDL933
C;Genetics:
A;Gene: Z4604
C;Superfamily: Escherichia coli hypothetical protein yhpP

Query Match 72.3%; Score 34; DB 2; Length 1266;
Best Local Similarity 66.7%; Pred. No. 1.9e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 TVSGNLTIR 9
:|||||
Db 1017 TISGNTLTL 1025

RESULT 10
P91143
hypothetical protein ECs4118 [imported] - Escherichia coli (strain O157:H7, substrain R
C;Species: Escherichia coli
C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004
C;Accession: F91143
R;Hayashi, T.; Makino, K.; Onishi, M.; Kurokawa, K.; Iehli, K.; Yokoyama, K.; Han, C.G
gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and gen
A;Reference number: A99629; MUID:21156231; PMID:11258796
A;Accession: F91143
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1266 <HAY>
A;Cross-references: UNIPROT:Q8X9D5; GB:BA000007; PIDN:BA837541.1; PID:gl3363591; GSPDB:
A;Experimental source: strain O157:H7, substrain RMD 0509952
C;Genetics:
A;Gene: ECs4118
C;Superfamily: Escherichia coli hypothetical protein yhpP

Query Match 72.3%; Score 34; DB 2; Length 1266;
Best Local Similarity 66.7%; Pred. No. 1.9e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 TVSGNLTIR 9
:|||||
Db 1017 TISGNTLTL 1025

RESULT 11
TPBPPI
tail fiber protein R - phage P1
C;Species: phage P1
C;Date: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 09-Jul-2004
C;Accession: JS0460
R;Guidolin, A.; Zingg, J.M.; Arber, W.
Gene 76, 239-243, 1989
A;Title: Organization of the bacteriophage P1 tail-fibre operon.
A;Reference number: PS0109; MUID:89326122; PMID:2526777
A;Accession: JS0460
A;Molecule type: DNA
A;Residues: 1-144 <GUI>
A;Cross-references: UNIPROT:P22946; GB:M25470; NID:g341349; PIDN:AAAS8777.1; PID:g538421
C;Genetics:
A;Gene: R
C;Superfamily: phage P1 tail fiber protein R
C;Keywords: tail fiber

Query Match 70.2%; Score 33; DB 1; Length 144;
Best Local Similarity 60.0%; Pred. No. 32;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 TVSGNLTIR 10
:|||||
Db 79 TYSGGIITVR 88

RESULT 12

S18683
gene R protein - Escherichia coli plasmid p15B
C:Species: Escherichia coli
C:Date: 03-May-1994 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C:Accession: S18683
R;Sandmeier, H.; Iida, S.; Huebner, P.; Hiestand-Nauer, R.; Arber, W.
Nucleic Acids Res. 19, 5831-5838, 1991
A:Title: Gene organization in the multiple DNA inversion region Min of plasmid p15B of E
A:Reference number: S18680; MUID:92051368; PMID:1945872
A:Accession: S18683
A:Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-144 <SAN>
A:Cross-references: UNIPROT:Q47426; EMBL:X62121; NID:g42224; PIDN:CAA44046.1; PID:g42228
C:Genetics:
A:Gene: R
A:Genome: plasmid
C:Superfamily: phage P1 tail fiber protein R

Query Match 70.2%; Score 33; DB 2; Length 144;
Best Local Similarity 60.0%; Pred. No. 32;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 TVSGNLTIR 10
| | | | | | | | | |

DB 79 TVSGGIITVR 88

RESULT 13

G95241
MATE efflux family protein [imported] - Streptococcus pneumoniae (strain TIGR4)
C:Species: Streptococcus pneumoniae
C:Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 09-Jul-2004
R;Tetzelin, H.; Nelson, K.E.; Paulsen, I.T.; Eissen, J.A.; Read, T.D.; Peterson, S.; Heid
on, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapfel,
nson, T.; Hickey, E.K.; Holt, I.E.
Science 293, 498-506, 2001
A:Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison,
A:Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae.
A:Reference number: A95000; MUID:21357209; PMID:11463916
A:Accession: G95241
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-411 <KUR>
A:Cross-references: UNIPROT:Q97NG5; GB:AE005672; PIDN:AAK76128.1; PID:g14973575; GSPDB:G
A:Experimental source: strain TIGR4
C:Genetics:
A:Gene: SP2065

Query Match 70.2%; Score 33; DB 2; Length 411;
Best Local Similarity 66.7%; Pred. No. 95;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 TVSGNLTIR 9
| | | | | | | | | |

DB 30 SVAGNIITI 38

RESULT 14

B98106
hypothetical protein MATE transporter [imported] - Streptococcus pneumoniae (strain R6)
C:Species: Streptococcus pneumoniae
C:Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 09-Jul-2004
C:Accession: B98106
R;Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszcak, L.; Burgett, S.; DeHoff, B.S.; B
e, R.; LeBlanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, S.; M
Y, P.; Sun, P.M.; Winkler, M.E.
J. Bacteriol. 183, 5709-5717, 2001
A:Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.R.;
A:Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.

A:Reference number: A97872; MUID:21429245; PMID:11544234

A:Accession: B98106
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-426 <KUR>
A:Cross-references: UNIPROT:Q8DN77; GB:AE007317; PIDN:AAL00679.1; PID:g15459568; GSPDB:G
C:Genetics:
A:Gene: MATE transporter

Query Match 70.2%; Score 33; DB 2; Length 426;
Best Local Similarity 66.7%; Pred. No. 98;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 TVSGNLTIR 9
| | | | | | | | | |

DB 45 SVAGNIITI 53

RESULT 15

F85253
hypothetical protein AT4g22170 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
C:Accession: F85253
R;anonymus, The European Union Arabidopsis Genome Sequencing Consortium, The Cold Sprin
Nature 402, 769-777, 1999
A:Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana.
A:Reference number: A85001; MUID:20083488; PMID:10617198
A:Accession: F85253
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-428 <STO>
A:Cross-references: UNIPROT:Q9SUG4; GB:NC_001268; NID:g7269062; PIDN:CAB79172.1; GSPDB:G
C:Genetics:
A:Gene: AT4g22170
A:Map position: 4
C:Superfamily: Arabidopsis thaliana hypothetical protein T12H17.50

Query Match 70.2%; Score 33; DB 2; Length 428;
Best Local Similarity 60.0%; Pred. No. 99;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 TVSGNLTIR 10
| | | | | | | | | |

DB 316 TVTGNILRVQ 325

Search completed: September 11, 2005, 01:43:55
Job time : 4.80952 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 11, 2005, 01:20:48 ; Search time 13.2381 Seconds
(without alignments)
386.822 Million cell updates/sec

Title: US-09-529-206E-4_COPY_127_136
Perfect score: 47
Sequence: 1 TVSGNLTIR 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Uniprot_03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	47	100.0	180	1 CTG1_HUMAN	P78358 homo sapien
2	40	85.1	141	2 Q67QW2	Q67QW2 symbiobacte
3	39	83.0	142	2 Q9NV13	Q9NV13 homo sapien
4	38	80.9	322	1 LIPA_RHET	O05941 rhizobium e
5	37	78.7	250	2 Q8G743	Q8G743 bifidobacte
6	36	76.6	245	2 Q64327	Q64327 bacterioph
7	36	76.6	318	2 Q8EAQ4	Q8EAQ4 shewanella
8	36	76.6	323	1 LIPA_AGR75	Q8UFG1 agrobacteri
9	36	76.6	352	2 Q9YH4	Q9YH4 lampetra fl
10	36	76.6	450	2 Q9R391	Q9R391 streptomyce
11	35	74.5	143	1 IBA2_HUMAN	Q14657 homo sapien
12	35	74.5	144	2 Q8A9J8	Q8A9J8 bacteroides
13	35	74.5	335	2 Q932F0	Q932F0 staphylococ
14	35	74.5	335	2 Q99VV7	Q99VV7 staphylococ
15	35	74.5	335	2 Q7A1K9	Q7A1K9 staphylococ
16	35	74.5	335	2 Q6GBG6	Q6GBG6 staphylococ
17	35	74.5	335	2 Q6GJ06	Q6GJ06 staphylococ
18	35	74.5	336	2 Q8CQ35	Q8CQ35 staphylococ
19	35	74.5	391	2 Q6LJS0	Q6LJS0 photobacter
20	35	74.5	674	2 Q6NRP9	Q6NRP9 xenopus lae
21	35	74.5	674	2 Q6NRP9	Q6NRP9 xenopus lae
22	35	74.5	674	2 Q9PT82	Q9PT82 xenopus lae
23	35	74.5	674	2 Q9PT82	Q9PT82 xenopus lae
24	35	74.5	742	2 Q8T4D0	Q8T4D0 drosophila
25	35	74.5	742	2 Q9V500	Q9V500 drosophila
26	35	74.5	907	2 Q9NEG0	Q9NEG0 drosophila
27	35	74.5	947	2 Q93FV1	Q93FV1 bacteroides
28	35	74.5	986	2 Q6C9K2	Q6C9K2 varrowia li
29	35	74.5	1086	2 Q8MSR5	Q8MSR5 drosophila
30	35	74.5	3215	2 Q8IRV7	Q8IRV7 drosophila
31	35	74.5	4117	2 Q8IRV9	Q8IRV9 drosophila

32	35	74.5	4179	2 Q9W4Y4	Q9W4Y4 drosophila
33	35	74.5	4223	2 Q8MPN3	Q8MPN3 drosophila
34	35	74.5	4228	2 Q8IRV8	Q8IRV8 drosophila
35	35	74.5	4684	2 Q6LJR7	Q6LJR7 photobacter
36	34	72.3	99	2 Q97675	Q97675 sus scrofa
37	34	72.3	131	1 FABA_PIG	Q97788 sus scrofa
38	34	72.3	177	1 RL6_BACST	P02391 bacillus st
39	34	72.3	244	1 IF6_SCHPO	O94476 schizosacch
40	34	72.3	305	2 Q8VGG6	Q8VGG6 mus musculu
41	34	72.3	311	2 Q8UJK3	Q8UJK3 agrobacteri
42	34	72.3	314	1 OR23_MOUSE	Q8V909 mus musculu
43	34	72.3	314	1 OR25_MOUSE	Q8V907 mus musculu
44	34	72.3	314	1 OR28_MOUSE	Q8V904 mus musculu
45	34	72.3	314	1 OR32_MOUSE	Q8Vfd2 mus musculu

ALIGNMENTS

RESULT 1

ID	CTG1_HUMAN	STANDARD;	PRT;	180 AA.
AC	P78358;			
DT	15-DEC-1998 (Rel. 37, Created)			
DT	15-DEC-1998 (Rel. 37, Last sequence update)			
DT	25-OCT-2004 (Rel. 45, Last annotation update)			
DE	Cancer/testis antigen 1B (Autoimmunogenic cancer/testis antigen NY-ESO-1)			
DE	ESO-1)			
GN	Name=CTAG1B; Synonyms=CTAG, CTAG1;			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]_TaxID=9606;			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=97203161; PubMed=9050879; DOI=10.1073/pnas.94.5.1914;			
RA	Chen Y.-T., Scanlan M.J., Sahin U., Tueraci O., Gure A.O., Teang S., Williamson B., Stockert E., Pfreundschuh M., Old L.J.;			
RA	"A testicular antigen aberrantly expressed in human cancers detected by autologous antibody screening."			
RT	Proc. Natl. Acad. Sci. U.S.A. 94:1914-1918(1997).			
RL	[2]			
RP	SEQUENCE FROM N.A.			
RX	TISSUE=Melanoma;			
RX	MEDLINE=98289662; PubMed=9626360;			
RA	Lethe B., Lucas S., Michaux L., de Smet C., Godelaine D., Serrano A., de Plaen E., Boon T.;			
RT	"LAGE-1, a new gene with tumor specificity."			
RL	Int. J. Cancer 76:903-908(1998).			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=98430682; PubMed=9759882;			
RA	Wang R.-F., Johnston S.L., Zeng G., Topalian S.L., Schwartzentruber D.J., Rosenberg S.A.;			
RT	"A breast and melanoma-shared tumor antigen: T cell responses to antigenic peptides translated from different open reading frames.";			
RL	J. Immunol. 161:3596-3606(1998).			
CC	-1- TISSUE SPECIFICITY: Expressed in testis and ovary and in a wide variety of cancers. Detected in uterine myometrium.			
CC	-1- SIMILARITY: Belongs to the CTAG family.			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).			
CC	EMBL: U87459; AAB49693.1; --			
DR	EMBL: A003149; CAA05908.1; --			
DR	EMBL: AF038567; AAD05202.1; --			
DR	Genew; HGNC:2491; CTAG1B.			

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DR MM; 300156; -.
KW Antigen; Transmembrane.
FT DOMAIN 5 82 Gly-rich.
FT TRANSMEM 156 172 Potential.
SQ SEQUENCE 180 AA; 17992 MW; B123C5C3C8BE1569 CRC64;

Query Match 100.0%; Score 47; DB 1; Length 180;
Best Local Similarity 100.0%; Pred. No. 0.3;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TVSGNLTIR 10
Db 127 TVSGNLTIR 136

RESULT 2
ID O67QW2 PRELIMINARY; PRT; 141 AA.
AC Q67QW2;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Hsp20 family heat shock protein.
GN ORFNames=STH946;
OS Symbiobacterium thermophilum.
OC Bacteria; Actinobacteria; Symbiobacterium.
OX NCBI_TaxID=2734;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=IAM14863;
RA Ueda K., Yanashita A., Ishikawa J., Shimada M., Watsuji T.,
RT Morimura K., Ikeda H., Hattori M., Beppu T.;
RT "Complete genome sequence of an uncultured bacterium Symbiobacterium
RT thermophilum.";
RL Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AP006940; BAD3931.1; -.
DR GO; GO:0006457; P:protein folding; IEA.
DR GO; GO:0006986; P:response to unfolded protein; IEA.
DR InterPro; IPR002068; Hsp20.
DR InterPro; IPR008978; HSP20_chap.
DR Pfam; PF00011; HSP20; 1.
DR PROSITE; PS01031; HSP20; 1.
KW Heat shock.
SQ SEQUENCE 141 AA; 15725 MW; C7BA8A8CFC50FD36 CRC64;

Query Match 85.1%; Score 40; DB 2; Length 141;
Best Local Similarity 80.0%; Pred. No. 6.2;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 TVSGNLTIR 10
Db 67 TVDGNLTIR 76

RESULT 3
Q9NY13
ID Q9NY13 PRELIMINARY; PRT; 142 AA.
AC Q9NY13;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Hypothetical protein LAGE-2 (Fragment).
GN Name=LAGE-2;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Lethe B.G.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ275978; CAB76945.1; -.
KW Hypothetical protein.

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FT NON_TER 1 1
SQ SEQUENCE 142 AA; 13895 MW; 27EBE922AC4ACC7B CRC64;

Query Match 83.0%; Score 39; DB 2; Length 142;
Best Local Similarity 88.9%; Pred. No. 10;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TVSGNLTIR 9
Db 101 TVSGNLTIR 109

RESULT 4
LIPA_RHIET
ID LIPA_RHIET STANDARD; PRT; 322 AA.
AC O05941;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Lipoyl synthase (EC 2.8.1.-) (Lipoic acid synthase) (Lipoate synthase)
DE (lipoyl-acyl-carrier protein synthase) (Sulfur insertion protein lipa)
DE (lip-syn).
GN Name=lipA;
OS Rhizobium etli.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Rhizobiaceae; Rhizobium/Agrobacterium group; Rhizobium.
OX NCBI_TaxID=29449;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CE3;
RX MEDLINE=97286510; PubMed=9141657; DOI=10.1016/S0378-1097(97)00069-4;
RA Tate R., Riccio A., Iaccarino M., Patriarca E.J.;
RT "Cloning and transcriptional analysis of the lipA (lipoic acid
RT synthetase) gene from Rhizobium etli.";
RL FEMS Microbiol. Lett. 149:165-172(1997).
CC -!- FUNCTION: Catalyzes the radical-mediated insertion of two sulfur
CC atoms into an acyl carrier protein (ACP) bound to an octanoyl
CC group to produce a lipoyl group (By similarity).
CC -!- CATALYTIC ACTIVITY: octanoyl-[acyl-carrier protein] + 2 sulfurs =
CC lipoyl-[acyl-carrier protein].
CC -!- COFACTOR: Binds 1 4Fe-4S cluster per subunit, and S-adenosyl-L-
CC methionine (AdoMet) used for 5'-deoxyadenosyl radical generation
CC (By similarity).
CC -!- PATHWAY: Lipoate biosynthesis; sulfur-insertion step.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -!- SIMILARITY: Belongs to the biotin and lipoic acid synthetases
CC family. LipA subfamily.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC
CC -----
CC EMBL; Y11708; CAA72400.1; -.
CC HAMAP; MF_00206; -.
CC InterPro; IPR006638; Elp3/MiaB/NifB.
CC InterPro; IPR003698; Lipoate synth.
CC InterPro; IPR007197; Radical SAM.
CC Pfam; PF04055; Radical SAM; 1.
CC SMART; SM00729; Elp3; 1.
CC TIGRFAMs; TIGR00510; lipA; 1.
CC 4Fe-4S; Iron; Iron-sulfur; Metal-binding; Transferase.
KW METAL 87 87 Iron-sulfur (Potential).
FT METAL 91 91 Iron-sulfur (Potential).
FT METAL 94 94 Iron-sulfur (Potential).
FT SEQUENCE 322 AA; 36297 MW; 45E7185215486847 CRC64;

Query Match 80.9%; Score 38; DB 1; Length 322;
Best Local Similarity 70.0%; Pred. No. 36;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

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QY 1 TVSGNLTIR 10
||:|||||:
Db 188 TVAGNLTIR 197

RESULT 5
Q8G743 ID Q8G743 PRELIMINARY; PRT; 250 AA.
AC Q8G743
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Possible cobyric acid synthase CobQ.
GN OrderedLocusNames=BL0429;
OS Bifidobacterium longum.
OC Bacteria; Actinobacteria; Actinobacteridae; Bifidobacteriales;
OC Bifidobacteriaceae; Bifidobacterium.
OX NCBI_TaxID=216816;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NCC 2705;
RX MEDLINE=22294977; PubMed=12381787; DOI=10.1073/pnas.212527599;
RA Schell M.A., Karmirantzou M., Snel B., Vilanova D., Berger B.,
RA Pessi G., Zwaheen M.-C., Desiere F., Bork P., Delley M.,
RA Pridmore R.D., Arigoni F.;
RT "The genome sequence of Bifidobacterium longum reflects its adaptation
RT to the human gastrointestinal tract."
RL Proc. Natl. Acad. Sci. U.S.A. 99:14422-14427(2002).
DR EMBL; AF014661; AN24266.1; -;
KW Complete proteome.
SQ SEQUENCE 250 AA; 27653 MW; 7577954A609689CF CRC64;

Query Match 78.7%; Score 37; DB 2; Length 250;
Best Local Similarity 87.5%; Pred. No. 45;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 SGNLTIR 10
||:|||||:
Db 21 SGNLTIR 28

RESULT 6
O64327 ID O64327 PRELIMINARY; PRT; 245 AA.
AC O64327
DT 01-AUG-1998 (TrEMBLrel. 07, Created)
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Gp13.
GN Names=gene 13;
OS Bacteriophage N15.
OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae;
OC Lambda-like viruses.
OX NCBI_TaxID=40631;
RN [1]
RP SEQUENCE FROM N.A.
RA Hendrix R.W., Ravin V.K., Casjens S.R., Ford M.E., Ravin N.V.,
RA Smirnov I.K.;
RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF064539; AAC19050.1; -;
DR PIR; T13099; T13099.
DR InterPro; IPR003343; Big_2.
DR InterPro; IPR008964; Invasin_intimin.
DR Pfam; PF02368; Big_2; 1.
DR SMART; SM00635; BID_2; 1.
SQ SEQUENCE 245 AA; 25571 MW; 2CC941997C103FD3 CRC64;

Query Match 76.6%; Score 36; DB 2; Length 245;
Best Local Similarity 77.8%; Pred. No. 71;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 TVSGNLTIR 9

Db 209 TVSGNLTIR 217

RESULT 7
Q8EAQ4 ID Q8EAQ4 PRELIMINARY; PRT; 318 AA.
AC Q8EAQ4
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical protein SO3842.
GN OrderedLocusNames=SO3842;
OS Shewanella oneidensis.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Alteromonadales;
OC Shewanellaceae; Shewanella.
OX NCBI_TaxID=70863;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NR-1;
RX MEDLINE=22297686; PubMed=12368813; DOI=10.1038/nbt749;
RA Heidelberg J.P., Paulsen I.T., Nelson K.E., Gaidos E.J., Nelson W.C.,
RA Read T.D., Eisen J.A., Seshadri R., Ward N.L., Methe B.A.,
RA Claydon R.A., Meyer T., Tsapin A., Scott J., Beanan M.J.,
RA Brinkac L.M., Daugherty S.C., DeBoy R.T., Dodson R.J., Durkin A.S.,
RA Haft D.H., Kolonay J.F., Madupu R., Peterson J.D., Umayam L.A.,
RA White O., Wolf A.M., Vamathevan J.J., Weidman J.F., Imbraim M.,
RA Lee K., Berry K.J., Lee C., Mueller J., Khouri H.M., Gill J.,
RA Utterback T.R., McDonald L.A., Feldblyum T.V., Smith H.O.,
RA Venter J.C., Neilson K.H., Fraser C.M.;
RT "Genome sequence of the dissimilatory metal ion-reducing bacterium
RT Shewanella oneidensis."
RL Nat. Biotechnol. 20:1118-1123(2002).
DR EMBL; AE015817; AN56819.1; -;
DR TIGR; SO3842; -;
KW Complete proteome.
SQ SEQUENCE 318 AA; 34113 MW; 0A0B7165033B6FCF CRC64;

Query Match 76.6%; Score 36; DB 2; Length 318;
Best Local Similarity 87.5%; Pred. No. 92;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TVSGNLTIR 8
||:|||||:
Db 153 TVSGNLTIR 160

RESULT 8
LIPA AGRTS ID LIPA AGRTS STANDARD; PRT; 323 AA.
AC Q8UFG1;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Lipoyl synthase (SC 2.8.1.-) (lipoyl acid synthase) (lipoate synthase)
DE (lipoyl-acyl-carrier protein synthase) (Sulfur insertion protein lipoA)
DE (lip-syn).
GN Name=lipoA; OrderedLocusNames=Atu1436, AGR_C.2646;
OS Agrobacterium tumefaciens (strain C58 / ATCC 33970).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Rhizobiaceae; Rhizobium/Agrobacterium group; Agrobacterium.
OX NCBI_TaxID=176299;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21608550; PubMed=11743193; DOI=10.1126/science.1065804;
RA Wood D.W., Setubal J.C., Kaul R., Monks D.E., Kitajima J.P.,
RA Okura Y.K., Zhou Y., Chen L., Wood G.E., Almeida N.F. Jr., Woo L.,
RA Chen Y., Paulsen I.T., Eisen J.A., Karp P.D., Bovee D. Sr.,
RA Chapman P., Clendenning J., Deatherage G., Gillet W., Grant C.,
RA Kutayvan T., Levy R., Li M.-J., McClelland E., Palmieri A., Gordon D.,
RA Raymond C., Rouse G., Saenphimachak C., Wu Z., Romero P., Perry M.,
RA Zhang S., Yoo H., Tao Y., Biddle P., Jung M., Krespan W., Dolan M.,
RA Gordon-Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan M.,

Putative odorant receptor LOR3.

OS Lampetra fluviatilis (River lamprey).

OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Hyperoartia;

OC Petromyzontiformes; Petromyzontidae; Lampetra.

NCBI_TaxID=7748;

[1]

RN SEQUENCE FROM N.A.

RP RC

PT TISSUE=Olfactory;

RX MEDLINE=9043746; PubMed=9828044;

RR DOI=10.1002/(SICI)1097-4695(19981115)37:3<383::AID-NEU4>3.3.CO;2-4;

RA Berghard A., Dryer L.;

RT "A novel family of ancient vertebrate odorant receptors.";

RL J. Neurobiol. 37:383-392(1998).

CC -1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).

CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.

DR EMBL; AF069546; AAC82381.1; -.

DR GO; GO:0016021; C:integral to membrane; IEA.

DR GO; GO:0004952; F:dopamine receptor activity; IEA.

DR GO; GO:0004872; F:receptor activity; IEA.

DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.

DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.

DR InterPro; IPR000925; Dopamine receptor.

DR InterPro; IPR000276; GPCR_Rhodpsn.

DR Pfam; PF00001; 7tm_1; 1.

DR PRINTS; PR00242; DOPAMINER.

DR PRINTS; PR00237; GPCRHHODOPSN.

DR PROSITE; PS00237; G_PROTEIN_REC FP 1; 1.

DR PROSITE; PS0262; G_PROTEIN_REC FP 2; 1.

DR G-protein coupled receptor; Receptor; Transmembrane.

SK SEQUENCE 352 AA; 40276 MW; 5366743DCFFA9FA4E CRC64;

Query Match 76.6%; Score 36; DB 2; Length 352;

Best Local Similarity 88.9%; Pred. No. 1e+02;

Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Cy 1 TVSGNIIIT 9

Db 45 TVVGNIIIT 53

RESULT 10

Q9RJ91 PRELIMINARY; PRT; 450 AA.

ID Q9RJ91 AC

DT 01-MAY-2000 (TrEMBLrel. 13, Created)

DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)

DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

DE Secretd endo-1,4-beta-xylanase (EC 3.2.1.18).

GN ORFNames=SCF91.34c;

OS Streptomyces coelicolor.

OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;

OC Streptomycinae; Streptomycetaceae; Streptomycetes.

OC NCBI_TaxID=1902;

[1]

RN SEQUENCE FROM N.A.

RP RC

PT STRAIN=A3(2) / M145;

RX MEDLINE=21996410; PubMed=12000953; DOI=10.1038/417141a;

RA Bentley S.D., Chater K.P., Cerdeno-Tarraga A.-M., Challis G.L.,

RA Thomson S.R., James K.D., Harris D.E., Quail M.A., Kieser H.,

RA Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,

RA Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,

RA Huang C.-H., Kieser T., Larke L., Murphy L.D., Oliver K., O'Neill S.,

RA Rabinowitz E., Rajandream M.A., Rutherford K.M., Rutter S.,

RA Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,

RA Warren T., Wietzorrek A., Woodward J.R., Barrell B.G., Parkhill J.,

RA Hopwood D.A.;

RT "Complete genome sequence of the model actinomycete Streptomyces

RT coelicolor A3(2).";

RL Nature 417:141-147(2002).

CC -1- SIMILARITY: Belongs to cellulase family F (family 10 of glycosyl

CC hydrolases).

DR EMBL; AL939106; CAB61191.1; -.

DR HSSP; P26514; 1E0W.

GO:	GO:0004553; F:hydrolase activity, hydrolyzing O-glycosyl . . .; IEA.
GO:	GO:0005975; P:carbohydrate metabolism; IEA.
GO:	InterPro: IPR001919; Bac_cellose-bind.
DR	InterPro: IPR008965; Cellul bind.
DR	InterPro: IPR001000; Glyco_hydro_10.
DR	Pfam: PF00553; CBM_2; 1.
DR	Pfam: PF00331; Glyco_hydro_10; 1.
DR	PRINTS: PR00134; GLHYDRLASE10.
DR	SMART: SM00637; CBD II; 1.
DR	SMART: SM00633; Glyco_10; 1.
DR	PROSITE: PS00591; GLYCOSYL HYDROL F10; 1.
KW	Complete proteome; Glycosidase; Hydrolase; Xylan degradation.
Q	SEQUENCE 450 AA; 47090 MW; E2FFA36EC29B6AE CRC64;
Query Match	76.6%; Score 36; DB 2; Length 450;
Best Local Similarity	60.0%; Pred. No. 1.3e+02;
Matches	6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
QY	1 TVSGNLTIR 10
DB	405 TWSGNVNTVR 414
RESULT 11	
IEA2_HUMAN	
ID	IEA2_HUMAN STANDARD; PRT; 143 AA.
AC	Q14657; Q81278;
DT	01-NOV-1997 (Rel. 35, Created)
DT	25-OCT-2004 (Rel. 45, Last sequence update)
DT	25-OCT-2004 (Rel. 45, Last annotation update)
DT	ITBA2 protein (BSO-3 protein) (DXS9879E).
DE	Name:ITBA2; Synonyms:ESO3;
GN	Homo sapiens (Human).
OS	Homo sapiens (Human).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX	NCBI_TaxID=9606;
RN	[1]
RP	SEQUENCE FROM N.A.
RP	TISSUE=Blood, and Pancreas;
RX	MEDLINE=223388257; PubMed=12477932; DOI=10.1073/pnas.2426038999;
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA	Klausner R.D., Collins F.S., Wagner L.H., Shenmen C.M., Schuler G.D.,
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heide F.,
RA	Diatchenko L., Marusina K., Farmer A.C., Rubin G.M., Hong L.,
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA	Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
RA	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA	Bosak S.A., McSwain P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA	Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA	Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA	Butterfield V.S.N., Krzywinski M.I., Skalska U., Smalls D.E.,
RA	Schmerer A., Schein J.E., Jones S.J.M., Matra M.A.;
RT	"Generation and initial analysis of more than 15,000 full-length human
RT	and mouse cDNA sequences.";
RL	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RL	[2]
RL	SEQUENCE OF 2-143 FROM N.A., AND TISSUE SPECIFICITY.
RC	TISSUE=Liver;
RX	MEDLINE=96374823; PubMed=8786131; DOI=10.1006/geno.1996.0293;
RA	Faranda S., Frattini A., Zucchi I., Patrosso C., Milanesi L.,
RA	Montagna C., Vezzoni P.;
RT	"Characterization and fine localization of two new genes in Xq28 using
RT	the genomic sequence/EST database screening approach.";
RL	Genomics 34:323-327 (1996).
RN	[3]
RP	IDENTIFICATION, AND TISSUE SPECIFICITY.
RX	PubMed=12384295;
RA	Alben B., Guere A.O., Scanlan M.J., Old L.J., Chen Y.-T.;

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DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Low-affinity inorganic phosphate transporter.
GN OrderedLocusNames=SAV0664;
OS Staphylococcus aureus (strain Mu50 / ATCC 700699).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=158878;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Mu50 / ATCC 700699;
RX MEDLINE=211311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T.,
RA Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
RA Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaio C.,
RA Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
RA Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
RT "Whole genome sequencing of methicillin-resistant Staphylococcus
RT aureus.";
RL Lancet 357:1225-1240(2001).
DR EMBL; AF003360; BAB56826.1; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005315; F:inorganic phosphate transporter activity; IEA.
DR GO; GO:0006817; P:phosphate transport; IEA.
DR InterPro; IPR001204; Phos_transporter.
DR Pfam; PF01384; PHO4; 1.
KW Complete proteome.
SQ SEQUENCE 335 AA; 35604 MW; 9135CAB8343FD628 CRC64;

Query Match 74.5%; Score 35; DB 2; Length 335;
Best Local Similarity 70.0%; Pred. No. 1.5e+02;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 TVSGNLTIR 10
DB 245 TVGGNIMKIR 254

RESULT 14
Q99VV7 PRELIMINARY; PRT; 335 AA.
AC Q99VV7;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE SA0619 protein.
GN OrderedLocusNames=SA0619;
OS Staphylococcus aureus (strain N315).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=158879;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=N315;
RX MEDLINE=211311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T.,
RA Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
RA Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaio C.,
RA Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
RA Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
RT "Whole genome sequencing of methicillin-resistant Staphylococcus
RT aureus.";
RL Lancet 357:1225-1240(2001).
DR EMBL; AF003360; BAB56826.1; -.
DR PIR; A89837; A89837.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005315; F:inorganic phosphate transporter activity; IEA.
DR GO; GO:0006817; P:phosphate transport; IEA.
DR InterPro; IPR001204; Phos_transporter.
DR Pfam; PF01384; PHO4; 1.
KW Complete proteome.
SQ SEQUENCE 335 AA; 35588 MW; 9121CBF8343FD628 CRC64;

Query Match 74.5%; Score 35; DB 2; Length 335;
Best Local Similarity 70.0%; Pred. No. 1.5e+02;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 TVSGNLTIR 10
DB 245 TVGGNIMKIR 254

RESULT 15
Q7AIK9 PRELIMINARY; PRT; 335 AA.
AC Q7AIK9;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE MW0626 protein.
GN OrderedLocusNames=MW0626;
OS Staphylococcus aureus (strain MW2).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=196620;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22040717; PubMed=12044378; DOI=10.1016/S0140-6736(02)08713-5;
RA Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A.,
RA Nagai Y., Iwama N., Asano K., Naimi T., Kuroda H., Cui L.,
RA Yamamoto K., Hiramatsu K.;
RT "Genome and virulence determinants of high virulence community-
RT acquired MRSA.";
RL Lancet 359:1819-1827(2002).
DR EMBL; AP004824; BAB94491.1; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005315; F:inorganic phosphate transporter activity; IEA.
DR GO; GO:0006817; P:phosphate transport; IEA.
DR InterPro; IPR001204; Phos_transporter.
DR Pfam; PF01384; PHO4; 1.
KW Complete proteome.
SQ SEQUENCE 335 AA; 35588 MW; 9121CBF8343FD628 CRC64;

Query Match 74.5%; Score 35; DB 2; Length 335;
Best Local Similarity 70.0%; Pred. No. 1.5e+02;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 TVSGNLTIR 10
DB 245 TVGGNIMKIR 254

Search completed: September 11, 2005, 01:42:53
Job time : 16.2381 secs

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OM protein - protein search, using sw model

Run on: September 11, 2005, 01:30:14 ; Search time 3.66667 Seconds
(without alignments)
203.588 Million cell updates/sec

Title: US-09-529-206E-4_COPY_127_136

Perfect score: 47
Sequence: 1 TVSGNLTIR 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
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6: /cgn2_6/prodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	47	100.0	18	3 US-09-359-503-9	Sequence 9, Appli
2	47	100.0	18	3 US-09-359-503-13	Sequence 13, Appli
3	47	100.0	18	4 US-09-165-546D-9	Sequence 9, Appli
4	47	100.0	18	4 US-09-165-546D-13	Sequence 13, Appli
5	47	100.0	18	4 US-09-408-036B-8	Sequence 8, Appli
6	47	100.0	18	4 US-09-408-036B-12	Sequence 12, Appli
7	47	100.0	180	2 US-08-791-495-9	Sequence 9, Appli
8	47	100.0	180	3 US-08-937-263B-8	Sequence 8, Appli
9	47	100.0	180	4 US-09-751-798-8	Sequence 8, Appli
10	47	100.0	180	4 US-09-392-714-25	Sequence 25, Appli
11	47	100.0	180	4 US-09-165-546D-15	Sequence 15, Appli
12	47	100.0	180	4 US-09-341-829A-9	Sequence 9, Appli
13	47	100.0	180	4 US-09-849-602-30	Sequence 30, Appli
14	42	89.4	9	4 US-09-344-040C-125	Sequence 125, App
15	42	89.4	9	4 US-09-833-039A-125	Sequence 125, App
16	38	80.9	9	4 US-09-344-040C-120	Sequence 120, App
17	38	80.9	9	4 US-09-833-039A-120	Sequence 120, App
18	38	80.9	180	2 US-08-791-495-7	Sequence 7, Appli
19	38	80.9	180	4 US-09-341-829A-7	Sequence 7, Appli
20	37	78.7	574	4 US-09-248-796A-16162	Sequence 16162, A
21	35	74.5	342	3 US-09-134-001C-5428	Sequence 5428, Ap
22	34	72.3	149	4 US-09-540-236-2614	Sequence 2614, Ap
23	34	72.3	177	4 US-09-732-210-1076	Sequence 1076, Ap
24	34	72.3	185	4 US-09-270-767-58027	Sequence 58027, A
25	34	72.3	379	4 US-09-270-767-42707	Sequence 42707, A
26	33	70.2	97	1 US-08-118-270-329	Sequence 329, App
27	33	70.2	97	5 PCT-US93-08528-329	Sequence 329, App

28 33 70.2 109 4 US-09-341-461-35 Sequence 35, Appli
29 33 70.2 362 3 US-09-134-001C-5209 Sequence 5209, Ap
30 33 70.2 379 1 US-08-118-270-32 Sequence 32, Appl
31 33 70.2 379 5 PCT-US93-08528-32 Sequence 32, Appl
32 33 70.2 426 4 US-09-583-110-4783 Sequence 4783, Ap
33 33 70.2 434 4 US-09-107-433-3247 Sequence 3247, Ap
34 33 70.2 470 3 US-09-292-071-25 Sequence 25, Appl
35 33 70.2 470 3 US-09-292-069A-25 Sequence 25, Appl
36 33 70.2 470 4 US-09-767-013-25 Sequence 25, Appl
37 33 70.2 470 4 US-09-292-072-25 Sequence 25, Appl
38 33 70.2 471 1 US-07-817-920-8 Sequence 8, Appli
39 33 70.2 471 1 US-07-996-772A-11 Sequence 11, Appl
40 33 70.2 471 1 US-08-370-542-7 Sequence 7, Appli
41 33 70.2 471 1 US-08-117-006-8 Sequence 8, Appli
42 33 70.2 471 1 US-08-216-594-8 Sequence 8, Appli
43 33 70.2 471 1 US-08-542-358-7 Sequence 7, Appli
44 33 70.2 471 2 US-08-244-434-2 Sequence 2, Appli
45 33 70.2 471 3 US-09-018-351-7 Sequence 7, Appli

ALIGNMENTS

RESULT 1
US-09-359-503-9
; Sequence 9, Application US/09359503
; Patent No. 6251603
; GENERAL INFORMATION:
; APPLICANT: Jager, Elke; Stockert, Elisabeth; Old, Lloyd J;
; APPLICANT: Knuth, alexander
; TITLE OF INVENTION: Method for Determining Status of A
; TITLE OF INVENTION: Cancerous Condition By Determining Antibodies
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fulbright & Jaworski, L.L.P.
; STREET: 666 Fifth Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: WordPerfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/359,503
; FILING DATE: July 23, 1999
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/165,546
; FILING DATE: October 2, 1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/062,422
; FILING DATE: April 17, 1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/937,263
; FILING DATE: September 15, 1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/752,182
; FILING DATE: 03-October-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, No. 6251603man D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: LUD 5466.1
; TELEPHONE: (212) 318-3000
; TELEFAX: (212) 752-5958
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid

to NY-

; TOPOLOGY: linear
US-09-359-503-9

Query Match 100.0%; Score 47; DB 3; Length 18;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 10; Conservative 0; Mismatches 0; Indels

Qy	1 TVSGNLTIR 10
Db	7 TVSGNLTIR 16

RESULT 2
 US-09-359-503-13
 ; Sequence 13, Application US/09359503
 ; Patent No. 6251603
 ; GENERAL INFORMATION:
 ; APPLICANT: Jager, Elke; Stockert, Elisabeth; Old, Lloyd J;
 ; APPLICANT: Knuth, alexander
 ; TITLE OF INVENTION: Method for Determining Status of A
 ; TITLE OF INVENTION: Cancerous Condition By Determining Antibodies
 ; TITLE OF INVENTION: a Patient Sample
 ; NUMBER OF SEQUENCES: 14
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Fulbright & Jaworski, L.L.P.

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Query Match      100.0%; Score 47; DB 3; Length 18;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 10: Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy	1	TVSGNLTIR	10
Db	1	TVSGNLTIR	10

Qy	1 TVSGNLTIR 10
D _b	7 TVSGNLTIR 16

; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10158
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Word
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/165,546D
; FILING DATE: 02-Oct-1998
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/062,422
; FILING DATE: April 17, 1998
; APPLICATION NUMBER: 08/937,263
; FILING DATE: September 15, 1997
; APPLICATION NUMBER: US 08/725,182
; FILING DATE: October 3, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, No. 6723832man D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: LUD 2166.4 CIP (09807811)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 318-3000
; TELEFAX: (212) 318-3400
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-09-165-546D-13

Query Match 100.0%; Score 47; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TVSGNLTIR 10
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DB 1 TVSGNLTIR 10
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RESULT 5
US-09-408-036B-8
; Sequence 8, Application US/09408036B
; Patent No. 6800730
; GENERAL INFORMATION:
; APPLICANT: Tureci, Ozlem
; APPLICANT: Sahin, Ugur
; TITLE OF INVENTION: Isolated Peptides Which Bind to MHC Class II Molecules and Uses
; FILE REFERENCE: LUD 5624
; CURRENT APPLICATION NUMBER: US/09/408,036B
; CURRENT FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: 09/344,040
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: 09/165,546
; PRIOR FILING DATE: 1998-10-02
; NUMBER OF SEQ ID NOS: 38
; SEQ ID NO 8
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-408-036B-8

Query Match 100.0%; Score 47; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TVSGNLTIR 10
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DB 7 TVSGNLTIR 16

RESULT 6

US-09-408-036B-12
; Sequence 12, Application US/09408036B
; Patent No. 6800730
; GENERAL INFORMATION:
; APPLICANT: Tureci, Ozlem
; APPLICANT: Sahin, Ugur
; APPLICANT: Pfreundschuh, Michael
; TITLE OF INVENTION: Isolated Peptides Which Bind to MHC Class II Molecules and Uses
; FILE REFERENCE: LUD 5624
; CURRENT APPLICATION NUMBER: US/09/408,036B
; CURRENT FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: 09/344,040
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: 09/165,546
; PRIOR FILING DATE: 1998-10-02
; NUMBER OF SEQ ID NOS: 38
; SEQ ID NO 12
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-408-036B-12

Query Match 100.0%; Score 47; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TVSGNLTIR 10
|||||

DB 1 TVSGNLTIR 10
|||||

RESULT 7

US-08-791-495-9
; Sequence 9, Application US/08791495
; Patent No. 5811519
; GENERAL INFORMATION:
; APPLICANT: Leth, Bernard
; APPLICANT: Lucas, Sophie
; APPLICANT: De Smet, Charles
; APPLICANT: Godelaine, Daniele
; APPLICANT: Boon-Falleur, Thierry
; TITLE OF INVENTION: LL-1 TUMOR SPECIFIC GENES
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wolf, Greenfield & Sacks, P.C.
; STREET: 600 Atlantic Avenue
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/791,495
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Van Amsterdam, John R.
; REGISTRATION NUMBER: 40,212
; REFERENCE/DOCKET NUMBER: L0461/7005
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-720-3500
; TELEFAX: 617-720-2441
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 180 amino acids

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; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-791-495-9

Query Match      100.0%; Score 47; DB 2; Length 180;
Best Local Similarity 100.0%; Pred. No. 0.15;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 TVSGNLTIR 10
Db      127 TVSGNLTIR 136

RESULT 8
US-08-937-263B-8
; Sequence 8, Application US/08937263B
; Patent No. 6274145
; GENERAL INFORMATION:
; APPLICANT: Chen, Yao-Tsang; Scanlan, Matthew;
; APPLICANT: Gure, Ali; Old, Lloyd J.; Jager, Elke;
; APPLICANT: Alexander, Knuth; Drifhout, Jan W.
; TITLE OF INVENTION: ISOLATED NUCLEIC ACID MOLECULE
; TITLE OF INVENTION: ENCODING CANCER ASSOCIATED ANTIGEN, THE ANTIGEN
; TITLE OF INVENTION: ITSELF, AND USES THEREOF
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fulbright & Jaworski, L.L.P.
; STREET: 666 Fifth Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: WordPerfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/937,263B
; FILING DATE: September 15, 1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/725,182
; FILING DATE: October 3, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Sinn, Eric, Patent Agent
; REGISTRATION NUMBER: 40,177
; REFERENCE/DOCKET NUMBER: LUD 5466.1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 318-3000
; TELEFAX: (212) 752-5958
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 180
; TYPE: amino acid
; TOPOLOGY: linear
US-08-937-263B-8

Query Match      100.0%; Score 47; DB 3; Length 180;
Best Local Similarity 100.0%; Pred. No. 0.15;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 TVSGNLTIR 10
Db      127 TVSGNLTIR 136

RESULT 9
US-09-751-798-8
; Sequence 8, Application US/09751798
; Patent No. 6525177
; GENERAL INFORMATION:
; APPLICANT: Stockert, Elisabeth; Jager, Elke;
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; APPLICANT: Chen, Yao-Tsang; Scanlan, Matthew;
; APPLICANT: Knuth, Alexander; Old, Lloyd J.
; TITLE OF INVENTION: Antibodies Which Bind to NY-ESO-1 Cancer
; MOLECULE TYPE: Truncated Forms of NY-ESO-1, and HLA
; TITLE OF INVENTION: Binding Peptides Derived Therefrom
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fulbright & Jaworski, L.L.P.
; STREET: 666 Fifth Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: WordPerfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/751,798
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/062,422
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/725,182
; FILING DATE: October 3, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, No. 6525177man D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: LUD 5466.3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 318-3168
; TELEFAX: (212) 752-5958
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 180
; TYPE: amino acid
; TOPOLOGY: linear
US-09-751-798-8

Query Match      100.0%; Score 47; DB 4; Length 180;
Best Local Similarity 100.0%; Pred. No. 0.15;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 TVSGNLTIR 10
Db      127 TVSGNLTIR 136

RESULT 10
US-09-392-714-25
; Sequence 25, Application US/09392714A
; Patent No. 6686147
; GENERAL INFORMATION:
; APPLICANT: Scanlan, Matthew J.
; APPLICANT: Gure, Ali O.
; APPLICANT: Williamson, Barbara
; APPLICANT: Chen, Yao-Tsang
; APPLICANT: Old, Lloyd J.
; TITLE OF INVENTION: Cancer Associated Antigens and Uses
; TITLE OF INVENTION: Therefor
; FILE REFERENCE: L0461/7062
; CURRENT APPLICATION NUMBER: US/09/392,714A
; CURRENT FILING DATE: 1999-09-09
; EARLIER APPLICATION NUMBER: PCT/US98/14679
; EARLIER FILING DATE: 1998-07-15
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 25
; LENGTH: 180
; TYPE: PRT
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; ORGANISM: Homo sapiens
US-09-392-714-25

Query Match      100.0%; Score 47; DB 4; Length 180;
Best Local Similarity 100.0%; Pred. No. 0.15;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 TVSGNLTIR 10
Db      127 TVSGNLTIR 136

RESULT 11
US-09-165-546D-15
; Sequence 15, Application US/09165546D
; Patent No. 6723832
; GENERAL INFORMATION:
; APPLICANT: Knuth, Alexander; Jager, Elke; Chen, Yao, Scanlan, Matt;
; Gure, Ali, Old, Lloyd, Ritter, Gerd
; TITLE OF INVENTION: ISOLATED PEPTIDES CORRESPONDING TO AMINO ACID
; SEQUENCES OF NY-ESO-1, WHICH BIND TO MHC CLASS I AND MHC CL
; USES THEREOF
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FULBRIGHT & JAWORSKI LLP
; STREET: 666 Fifth Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10158
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Word
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/165,546D
; FILING DATE: 02-Oct-1998
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/062,422
; FILING DATE: April 17, 1998
; APPLICATION NUMBER: 08/937,263
; FILING DATE: September 15, 1997
; APPLICATION NUMBER: US 08/725,182
; FILING DATE: October 3, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, No. 6723832man D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: LUD 2166.4 CIP (09807811)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 318-3000
; TELEFAX: (212) 318-3400
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 180 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 15
US-09-165-546D-15

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Best Local Similarity 100.0%; Pred. No. 0.15;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 TVSGNLTIR 10
Db      127 TVSGNLTIR 136

RESULT 12
US-09-341-829A-9
; Sequence 9, Application US/09341829A
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; Patent No. 6794131
; GENERAL INFORMATION:
; APPLICANT: Leth,, Bernard
; APPLICANT: Lucas, Sophie
; APPLICANT: De Smet, Charles
; APPLICANT: Godelaine, Daniele
; APPLICANT: Boon-Falleur, Thierry
; TITLE OF INVENTION: LAGE-1 TUMOR ASSOCIATED NUCLEIC ACIDS
; FILE REFERENCE: L0461/7066
; CURRENT APPLICATION NUMBER: US/09/341,829A
; CURRENT FILING DATE: 1999-10-18
; PRIOR APPLICATION NUMBER: US 08/791,495
; PRIOR APPLICATION NUMBER: PCT/US98/01445
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 9
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-341-829A-9

Query Match      100.0%; Score 47; DB 4; Length 180;
Best Local Similarity 100.0%; Pred. No. 0.15;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 TVSGNLTIR 10
Db      127 TVSGNLTIR 136

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US-09-849-602-30
; Sequence 30, Application US/09849602
; Patent No. 6794501
; GENERAL INFORMATION:
; APPLICANT: Scanlan, Matthew J.
; APPLICANT: Old, Lloyd J.
; APPLICANT: Stockert, Elisabeth
; APPLICANT: Chen, Yao-Tseung
; TITLE OF INVENTION: Colon Cancer Antigen Panel
; FILE REFERENCE: L0461/7105 (JRV)
; CURRENT APPLICATION NUMBER: US/09/849,602
; CURRENT FILING DATE: 2001-05-04
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 30
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-849-602-30

Query Match      100.0%; Score 47; DB 4; Length 180;
Best Local Similarity 100.0%; Pred. No. 0.15;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 TVSGNLTIR 10
Db      127 TVSGNLTIR 136

RESULT 14
US-09-344-040C-125
; Sequence 125, Application US/09344040C
; Patent No. 6548064
; GENERAL INFORMATION:
; APPLICANT: Tureci, Ozlem
; APPLICANT: Sahin, Ugur
; APPLICANT: Pfrendschuh, Michael
; APPLICANT: Ramensee, Hans Georg
; APPLICANT: Stevanovic, Stefan
; TITLE OF INVENTION: Method for Determining Presence of Cancer In a Sample By Determini
; TITLE OF INVENTION: Expression of an SSX Gene, Peptides Derived From Said SSX Gene
; TITLE OF INVENTION: Gene, and Uses Thereof
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; FILE REFERENCE: LUD 5556.1
; CURRENT APPLICATION NUMBER: US/09/344,040C
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: US 09/105,839
; PRIOR FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: US 08/851,130
; PRIOR FILING DATE: 1997-05-05
; NUMBER OF SEQ ID NOS: 132
; SEQ ID NO 125
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-344-040C-125

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Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TVSGNILTI 9
Db 1 TVSGNILTI 9

RESULT 15

US-09-833-039A-125
; Sequence 125, Application US/09833039A
; Patent No. 6673350
; GENERAL INFORMATION:
; APPLICANT: Tureci, Ozlem
; APPLICANT: Sahin, Ugur
; APPLICANT: Pfreundschuh, Michael
; TITLE OF INVENTION: Tumor Associated Peptide and Uses Thereof
; FILE REFERENCE: LUD 5622.1
; CURRENT APPLICATION NUMBER: US/09/833,039A
; CURRENT FILING DATE: 2001-04-12
; PRIOR APPLICATION NUMBER: US 09/409,455
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: US 09/344,040
; PRIOR FILING DATE: 1999-06-26
; PRIOR APPLICATION NUMBER: US 09/105,839
; PRIOR FILING DATE: 1998-06-26
; NUMBER OF SEQ ID NOS: 131
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 125
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-833-039A-125

Query Match 89.4%; Score 42; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TVSGNILTI 9
Db 1 TVSGNILTI 9

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 11, 2005, 01:43:05 ; Search time 13.5238 Seconds
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291.657 Million cell updates/sec

Title: US-09-529-206E-4_COPY_127_136

Perfect score: 47 TVSGNLTIR 10

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Searched: 1777461 seqs, 394431504 residues

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Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	47	100.0	15	18	US-10-182-506A-15
3	47	100.0	15	18	US-10-182-506A-16
4	47	100.0	18	16	US-10-751-088-9
5	47	100.0	18	16	US-10-751-088-13
6	47	100.0	18	16	US-10-851-884-8
7	47	100.0	18	16	US-10-851-884-12
8	47	100.0	18	18	US-10-182-506A-65
9	47	100.0	20	15	US-10-164-121A-35
10	47	100.0	20	15	US-10-164-078A-34
11	47	100.0	20	18	US-10-182-506A-38
					Sequence 17, Appl
					Sequence 15, Appl
					Sequence 16, Appl
					Sequence 9, Appl
					Sequence 13, Appl
					Sequence 8, Appl
					Sequence 12, Appl
					Sequence 65, Appl
					Sequence 35, Appl
					Sequence 34, Appl
					Sequence 38, Appl

12	47	100.0	25	17	US-10-491-891-83	Sequence 83, Appl
13	47	100.0	27	18	US-10-182-506A-7	Sequence 7, Appl
14	47	100.0	27	18	US-10-182-506A-6	Sequence 6, Appl
15	47	100.0	30	15	US-10-296-734-1414	Sequence 1414, Ap
16	47	100.0	54	15	US-10-447-161-140	Sequence 140, App
17	47	100.0	123	16	US-10-777-053-17	Sequence 17, Appl
18	47	100.0	123	16	US-10-837-217-17	Sequence 20, Appl
19	47	100.0	179	16	US-10-777-053-20	Sequence 20, Appl
20	47	100.0	179	16	US-10-837-217-20	Sequence 20, Appl
21	47	100.0	179	17	US-10-482-029-202	Sequence 202, App
22	47	100.0	180	9	US-09-751-798-8	Sequence 8, Appl
23	47	100.0	180	10	US-09-849-602-30	Sequence 30, Appl
24	47	100.0	180	13	US-10-023-182-8	Sequence 8, Appl
25	47	100.0	180	14	US-10-207-655-71	Sequence 71, Appl
26	47	100.0	180	15	US-10-036-066-3	Sequence 3, Appl
27	47	100.0	180	15	US-10-117-937-74	Sequence 74, Appl
28	47	100.0	180	15	US-10-285-027-386	Sequence 386, App
29	47	100.0	180	15	US-10-296-734-832	Sequence 832, App
30	47	100.0	180	15	US-10-188-832-139	Sequence 139, App
31	47	100.0	180	16	US-10-777-053-11	Sequence 11, Appl
32	47	100.0	180	16	US-10-751-088-15	Sequence 15, Appl
33	47	100.0	180	16	US-10-657-022-74	Sequence 74, Appl
34	47	100.0	180	16	US-10-837-217-11	Sequence 11, Appl
35	47	100.0	180	16	US-10-877-373-9	Sequence 9, Appl
36	47	100.0	180	16	US-10-723-860-1270	Sequence 1270, Ap
37	47	100.0	180	17	US-10-871-708-7	Sequence 7, Appl
38	47	100.0	180	18	US-10-895-523-3	Sequence 3, Appl
39	47	100.0	180	18	US-10-182-506A-3	Sequence 3, Appl
40	47	100.0	180	18	US-10-756-149-5024	Sequence 5024, Ap
41	47	100.0	180	20	US-11-067-064-74	Sequence 74, Appl
42	47	100.0	397	9	US-09-821-883-27	Sequence 27, Appl
43	47	100.0	3541	15	US-10-296-734-1454	Sequence 1454, Ap
44	42	89.4	9	10	US-09-833-039-125	Sequence 125, App
45	42	89.4	9	14	US-10-177-277-125	Sequence 125, App

ALIGNMENTS

RESULT 1

US-10-182-506A-17

; Sequence 17, Application US/10182506A

; Publication No. US20050136402A1

; GENERAL INFORMATION:

; APPLICANT: Wang, R-F

; APPLICANT: Rosenberg, S A

; APPLICANT: Zeng, G

; TITLE OF INVENTION: NOVEL MHC CLASS II RESTRICTED T CELL EPITOPES FROM THE CANCER

; FILE REFERENCE: 217955

; CURRENT APPLICATION NUMBER: US/10/182,506A

; PRIOR FILING DATE: 2002-10-28

; PRIOR APPLICATION NUMBER: PCT/US01/02765

; PRIOR FILING DATE: 2001-01-26

; PRIOR APPLICATION NUMBER: 60/179,004

; PRIOR FILING DATE: 2000-01-28

; PRIOR APPLICATION NUMBER: 60/237,107

; PRIOR FILING DATE: 2000-09-29

; NUMBER OF SEQ ID NOS: 80

; SOFTWARE: Patentin version 3.1

; SEQ ID NO 17

; LENGTH: 14

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Synthetic

US-10-182-506A-17

Query Match 100.0%; Score 47; DB 18; Length 14;

Best Local Similarity 100.0%; Pred. No. 0.026; Indels 0; Gaps 0;

Matches 10; Conservative 0; Mismatches 0;

QY 1 TVSGNLTIR 10

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Db          |||||
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RESULT 2
US-10-182-506A-15
; Sequence 15, Application US/10182506A
; Publication No. US20050136402A1
; GENERAL INFORMATION:
; APPLICANT: Wang, R-F
; APPLICANT: Rosenberg, S A
; APPLICANT: Zeng, G
; TITLE OF INVENTION: NOVEL MHC CLASS II RESTRICTED T CELL EPITOPES FROM THE CANCER
; FILE REFERENCE: 217955
; CURRENT APPLICATION NUMBER: US/10/182,506A
; CURRENT FILING DATE: 2002-10-28
; PRIOR APPLICATION NUMBER: PCT/US01/02765
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 60/179,004
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: 60/237,107
; PRIOR FILING DATE: 2000-09-29
; NUMBER OF SEQ ID NOS: 80
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 15
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-182-506A-15

Query Match          100.0%; Score 47; DB 18; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.029;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          1 TVSGNLTIR 10
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Db          6 TVSGNLTIR 15

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; Sequence 16, Application US/10182506A
; Publication No. US20050136402A1
; GENERAL INFORMATION:
; APPLICANT: Wang, R-F
; APPLICANT: Rosenberg, S A
; APPLICANT: Zeng, G
; TITLE OF INVENTION: NOVEL MHC CLASS II RESTRICTED T CELL EPITOPES FROM THE CANCER
; FILE REFERENCE: 217955
; CURRENT APPLICATION NUMBER: US/10/182,506A
; CURRENT FILING DATE: 2002-10-28
; PRIOR APPLICATION NUMBER: PCT/US01/02765
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 60/179,004
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: 60/237,107
; PRIOR FILING DATE: 2000-09-29
; NUMBER OF SEQ ID NOS: 80
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 16
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-182-506A-16

Query Match          100.0%; Score 47; DB 18; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.029;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db          4 TVSGNLTIR 13
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Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db          5 TVSGNLTIR 14

RESULT 4
US-10-751-088-9
; Sequence 9, Application US/10751088
; Publication No. US20040158044A1
; GENERAL INFORMATION:
; APPLICANT: Knuth, Alexander; Jager, Elke; Chen, Yao, Scanlan, Matt;
; TITLE OF INVENTION: ISOLATED PEPTIDES CORRESPONDING TO AMINO ACID
; SEQUENCES OF NY-ESO-1, WHICH BIND TO MHC CLASS I AND MHC CI.
; USES THEREOF
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FULBRIGHT & JAWORSKI LLP
; STREET: 666 Fifth Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10158
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Word
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/751,088
; FILING DATE: 02-Jan-2004
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/165,546D
; FILING DATE: 02-Oct-1998
; APPLICATION NUMBER: 09/062,422
; FILING DATE: April 17, 1998
; APPLICATION NUMBER: 08/937,263
; FILING DATE: September 15, 1997
; APPLICATION NUMBER: US 08/725,182
; FILING DATE: October 3, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, Norman D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: LUD 2166.4 CIP (09807811)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 318-3000
; TELEFAX: (212) 318-3400
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-10-751-088-9

Query Match          100.0%; Score 47; DB 16; Length 18;
Best Local Similarity 100.0%; Pred. No. 0.035;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          1 TVSGNLTIR 10
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Db          7 TVSGNLTIR 16

RESULT 5
US-10-751-088-13
; Sequence 13, Application US/10751088
; Publication No. US20040158044A1
; GENERAL INFORMATION:
; APPLICANT: Knuth, Alexander; Jager, Elke; Chen, Yao, Scanlan, Matt;
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; Gure, Ali, Old, Lloyd, Ritter, Gerd
; TITLE OF INVENTION: ISOLATED PEPTIDES CORRESPONDING TO AMINO ACID
; SEQUENCES OF NY-ESO-1, WHICH BIND TO MHC CLASS I AND MHC CI
; USES THEREOF
;
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FULBRIGHT & JAWORSKI LLP
; STREET: 666 Fifth Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10158
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Word
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/751,088
; FILING DATE: 02-Jan-2004
; CLASSIFICATION: 530
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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/165,546D
; FILING DATE: 02-Oct-1998
; APPLICATION NUMBER: 09/062,422
; FILING DATE: April 17, 1998
; APPLICATION NUMBER: 08/937,263
; FILING DATE: September 15, 1997
; APPLICATION NUMBER: US 08/725,182
; FILING DATE: October 3, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, Norman D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: LUD 2166.4 CIP (09807811)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 318-3000
; TELEFAX: (212) 318-3400
;
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TOPOLOGY: linear
;
; SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-10-751-088-13

Query Match 100.0%; Score 47; DB 16; Length 18;
Best Local Similarity 100.0%; Pred. No. 0.035;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 TVSGNLTIR 10

RESULT 6
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; Publication No. US20040214284A1
; GENERAL INFORMATION:
; APPLICANT: Sahin, Ugur
; APPLICANT: Pfreundschuh, Michael
; TITLE OF INVENTION: Isolated Peptides Which Bind to MHC Class II Molecules and Uses T
; FILE REFERENCE: LUD 5624
; CURRENT APPLICATION NUMBER: US/10/851,884
; CURRENT FILING DATE: 2004-05-21
; PRIOR APPLICATION NUMBER: US/09/408,036
; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: 09/344,040
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: 09/165,546
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn version 3.1
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; TYPE: PRT
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; NUMBER OF SEQ ID NOS: 38
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; LENGTH: 18
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-851-884-8

Query Match 100.0%; Score 47; DB 16; Length 18;
Best Local Similarity 100.0%; Pred. No. 0.035;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TVSGNLTIR 10
Db 7 TVSGNLTIR 16

RESULT 7
US-10-851-884-12
; Sequence 12, Application US/10851884
; Publication No. US20040214284A1
; GENERAL INFORMATION:
; APPLICANT: Tureci, Ozlem
; APPLICANT: Sahin, Ugur
; APPLICANT: Pfreundschuh, Michael
; TITLE OF INVENTION: Isolated Peptides Which Bind to MHC Class II Molecules and Uses
; FILE REFERENCE: LUD 5624
; CURRENT APPLICATION NUMBER: US/10/851,884
; CURRENT FILING DATE: 2004-05-21
; PRIOR APPLICATION NUMBER: US/09/408,036
; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: 09/344,040
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: 09/165,546
; PRIOR FILING DATE: 1998-10-02
; NUMBER OF SEQ ID NOS: 38
; SEQ ID NO 12
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-851-884-12

Query Match 100.0%; Score 47; DB 16; Length 18;
Best Local Similarity 100.0%; Pred. No. 0.035;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TVSGNLTIR 10
Db 1 TVSGNLTIR 10

RESULT 8
US-10-182-506A-65
; Sequence 65, Application US/10182506A
; Publication No. US20050136402A1
; GENERAL INFORMATION:
; APPLICANT: Wang, R-F
; APPLICANT: Rosenberg, S A
; APPLICANT: Zeng, G
; TITLE OF INVENTION: NOVEL MHC CLASS II RESTRICTED T CELL EPITOPES FROM THE CANCER
; FILE REFERENCE: 217955
; CURRENT APPLICATION NUMBER: US/10/182,506A
; CURRENT FILING DATE: 2002-10-28
; PRIOR APPLICATION NUMBER: PCT/US01/02765
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 60/179,004
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: 60/237,107
; PRIOR FILING DATE: 2000-09-29
; NUMBER OF SEQ ID NOS: 80
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 65
; LENGTH: 18
; TYPE: PRT
;
; NUMBER OF SEQ ID NOS: 38
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; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-182-506A-65

Query Match 100.0%; Score 47; DB 18; Length 18;
Best Local Similarity 100.0%; Pred. No. 0.035; Indels 0; Gaps 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TVSGNLTIR 10
Db 7 TVSGNLTIR 16
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RESULT 9

US-10-164-121A-35
; Sequence 35, Application US/10164121A
; Publication No. US20030228308A1
; GENERAL INFORMATION:
; APPLICANT: Zhang, Yi
; APPLICANT: Boon, Thierry
; APPLICANT: Van der Bruggen, Pierre
; APPLICANT: Traversari, Catra
; TITLE OF INVENTION: Isolated Peptides Which Bind to HLA-Cw6 Molecules And Uses Thereof
; FILE REFERENCE: LUD-5771
; CURRENT APPLICATION NUMBER: US/10/164,121A
; CURRENT FILING DATE: 2002-08-26
; NUMBER OF SEQ ID NOS: 36
; SEQ ID NO 35
; LENGTH: 20
; TYPE: PRT
; ORGANISM: H. sapiens
; FEATURE:
US-10-164-121A-35

Query Match 100.0%; Score 47; DB 15; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.039;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TVSGNLTIR 10
Db 9 TVSGNLTIR 18
|||||

RESULT 10

US-10-164-078A-34
; Sequence 34, Application US/10164078A
; Publication No. US20030228325A1
; GENERAL INFORMATION:
; APPLICANT: Bilsborough, Janine
; APPLICANT: Schultz, Erwin
; APPLICANT: Panichelli, Christophe
; APPLICANT: Van der Bruggen, Pierre
; APPLICANT: Boon, Thierry
; TITLE OF INVENTION: Isolated Peptides Which Bind to HLA-B18 Molecules And Uses Thereof
; FILE REFERENCE: LUD-5756
; CURRENT APPLICATION NUMBER: US/10/164,078A
; CURRENT FILING DATE: 2002-06-05
; NUMBER OF SEQ ID NOS: 35
; SEQ ID NO 34
; LENGTH: 20
; TYPE: PRT
; ORGANISM: H. sapiens
; FEATURE:
US-10-164-078A-34

Query Match 100.0%; Score 47; DB 15; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.039;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TVSGNLTIR 10
Db 9 TVSGNLTIR 18
|||||

RESULT 11
US-10-182-506A-38
; Sequence 38, Application US/10182506A
; Publication No. US20050136402A1
; GENERAL INFORMATION:
; APPLICANT: Wang, R-F
; APPLICANT: Rosenberg, S A
; APPLICANT: Zeng, G
; TITLE OF INVENTION: NOVEL MHC CLASS II RESTRICTED T CELL EPITOPES FROM THE CANCER
; TITLE OF INVENTION: ANTIGEN, NY ESO-1
; FILE REFERENCE: 217955
; CURRENT APPLICATION NUMBER: US/10/182,506A
; CURRENT FILING DATE: 2002-10-28
; PRIOR APPLICATION NUMBER: PCT/US01/02765
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 60/179,004
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: 60/237,107
; PRIOR FILING DATE: 2000-09-29
; NUMBER OF SEQ ID NOS: 80
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 38
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-182-506A-38

Query Match 100.0%; Score 47; DB 18; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.039; Indels 0; Gaps 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TVSGNLTIR 10
Db 2 TVSGNLTIR 11
|||||

RESULT 12

US-10-491-891-83
; Sequence 83, Application US/10491891
; Publication No. US20050059107A1
; GENERAL INFORMATION:
; APPLICANT: MAILLERE, BERNARD
; APPLICANT: CASTELLI, FLORENCE
; APPLICANT: BUHOT, CECILE
; APPLICANT: GEORGES, BERTRAND
; TITLE OF INVENTION: METHOD OF SELECTING HLA-DP4 LIGANDS AND THE APPLICATIONS THEREOF
; FILE REFERENCE: 251858USOXPT
; CURRENT APPLICATION NUMBER: US/10/491,891
; CURRENT FILING DATE: 2004-04-15
; PRIOR APPLICATION NUMBER: PCT/FR02/03555
; PRIOR FILING DATE: 2002-10-17
; PRIOR APPLICATION NUMBER: FR01/13352
; PRIOR FILING DATE: 2001-10-17
; NUMBER OF SEQ ID NOS: 129
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 83
; LENGTH: 25
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: SYNTHETIC PEPTIDE
US-10-491-891-83

Query Match 100.0%; Score 47; DB 17; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.051; Indels 0; Gaps 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TVSGNLTIR 10
|||||

Db 9 TVSGNLTIR 18

RESULT 13
US-10-182-506A-7
; Sequence 7, Application US/10182506A
; Publication No. US20050136402A1
; GENERAL INFORMATION:
; APPLICANT: Wang, R-F
; APPLICANT: Rosenberg, S A
; APPLICANT: Zeng, G
; TITLE OF INVENTION: NOVEL MHC CLASS II RESTRICTED T CELL EPITOPES FROM THE CANCER
; TITLE OF INVENTION: ANTIGEN, NY ESO-1
; FILE REFERENCE: 217955
; CURRENT APPLICATION NUMBER: US/10/182,506A
; PRIOR FILING DATE: 2002-10-28
; PRIOR APPLICATION NUMBER: PCT/US01/02765
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 60/179,004
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: 60/237,107
; PRIOR FILING DATE: 2000-09-29
; NUMBER OF SEQ ID NOS: 80
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 25
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-182-506A-7

Query Match 100.0%; Score 47; DB 18; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.051;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TVSGNLTIR 10

Db 15 TVSGNLTIR 24

RESULT 14
US-10-182-506A-6
; Sequence 6, Application US/10182506A
; Publication No. US20050136402A1
; GENERAL INFORMATION:
; APPLICANT: Wang, R-F
; APPLICANT: Rosenberg, S A
; APPLICANT: Zeng, G
; TITLE OF INVENTION: NOVEL MHC CLASS II RESTRICTED T CELL EPITOPES FROM THE CANCER
; TITLE OF INVENTION: ANTIGEN, NY ESO-1
; FILE REFERENCE: 217955
; CURRENT APPLICATION NUMBER: US/10/182,506A
; CURRENT FILING DATE: 2002-10-28
; PRIOR APPLICATION NUMBER: PCT/US01/02765
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 60/179,004
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: 60/237,107
; PRIOR FILING DATE: 2000-09-29
; NUMBER OF SEQ ID NOS: 80
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 27
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-182-506A-6

Query Match 100.0%; Score 47; DB 18; Length 27;
Best Local Similarity 100.0%; Pred. No. 0.055;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TVSGNLTIR 10

Db 17 TVSGNLTIR 26

RESULT 15
US-10-296-734-1414
; Sequence 1414, Application US/10296734
; Publication No. US20040054137A1
; GENERAL INFORMATION:
; APPLICANT: Thompson, Scott A
; APPLICANT: Ramshaw, Ian A
; TITLE OF INVENTION: Synthetic molecules and uses therefor
; FILE REFERENCE: Savine
; CURRENT APPLICATION NUMBER: US/10/296,734
; CURRENT FILING DATE: 2003-08-04
; PRIOR APPLICATION NUMBER: AU PQ7761/00
; PRIOR FILING DATE: 2000-05-26
; NUMBER OF SEQ ID NOS: 1507
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1414
; LENGTH: 30
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: NYSOLA segment 9
US-10-296-734-1414

Query Match 100.0%; Score 47; DB 15; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.062;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TVSGNLTIR 10

Db 9 TVSGNLTIR 18

Search completed: September 11, 2005, 02:07:11
Job time : 14.5238 secs

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